129789

From:	Yaen, Christopher
Sent:	Thursday, August 12, 2004 2:59 PM
To:	STIC-Biotech/ChemLib
Subject:	09/889300

could you run a regular search and an interference search on seq id 1 and 2

thanks

Christopher Yaen
US Patent Office
Art Unit 1642
571-272-0838
REM 3A20
REM 3C18

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SEARCH REQUEST FORM

Requestor's
Name: _____

Serial
Number: _____

Date: _____   Phone: _____   Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

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Date completed: 08-10-04	**Search Site**	**Vendors**
Searcher: Besera, C 2578	_____ STIC	_____ IG
Terminal time: 20	_____ CM-1	_____ STN
Elapsed time: _____	_____ Pre-S	_____ Dialog
CPU time: _____	**Type of Search**	_____ APS
Total time: 25	_____ N.A. Sequence	_____ Geninfo
Number of Searches: _____	_____ A.A. Sequence	_____ SDC
Number of Databases: 1	_____ Structure	_____ DARC/Questel
	_____ Bibliographic	✓ Other CGN

PTO-1590 (9-90)

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CM protein - protein search, using sw model

Run on:   August 16, 2004, 11:08:06 ; Search time 50.4574 Seconds
                                       (without alignments)
                                       649.568 Million cell updates/sec

Title:          US-09-889-300A-1
Perfect score:  614
Sequence:       1 QVQLQQSGAELVRPGTSVKV.........ARDGPWFAYWGQGTLVTVSA 116
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:     1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    A_Geneseq_29Jan04:*
              1: geneseqp1980s:*
              2: geneseqp1990s:*
              3: geneseqp2000s:*
              4: geneseqp2001s:*
              5: geneseqp2002s:*
              6: geneseqp2003as:*
              7: geneseqp2003bs:*
              8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	614	100.0	116	3	AAB10443	Aab10443 Murine mo
2	554.5	90.3	119	3	AAW49814	Aaw49814 Amino aci
3	554.5	90.3	119	6	ABR55869	Abr55869 Anti-glyc
4	554.5	90.3	138	2	AAR39266	Aar39266 Mouse C4G
5	554.5	90.3	138	2	AAW49810	Aaw49810 Variable
6	546.5	89.0	119	2	AAW01580	Aaw01580 Lead bind
7	519	84.5	138	6	AAE34367	Aae34367 Escherich
8	517.5	84.3	164	5	ABG71533	Abg71533 Mouse ant
9	515	83.9	137	2	AAR12360	Aar12360 Heavy cha
10	515	83.9	137	2	AAR12238	Aar12238 Mouse MAb
11	515	83.9	141	2	AAR09427	Aar09427 ME4 Heavy
12	515	83.9	141	2	AAW06216	Aaw06216 MAb ME4 h
13	515	83.9	141	6	AAW85063	Aaw85063 Mouse ME4
14	515	83.9	141	2	ABU58897	Abu58897 Mouse ant
15	510.5	83.1	138	2	AAW34515	Aaw34515 Variable
16	503.5	82.0	119	2	AAW49813	Aaw49813 Amino aci
17	503.5	82.0	119	6	ABR55868	Abr55868 Human imm
18	503.5	82.0	121	2	AAW07437	Aaw07437 Anti-DNA
19	503.5	82.0	222	2	AAR39267	Aar39267 Humanised
20	503.5	82.0	222	2	AAW49817	Aaw49817 Fragment
21	503.5	82.0	235	2	AAR39268	Aar39268 Humanised
22	503.5	82.0	235	2	AAW49818	Aaw49818 Amino aci
23	503.5	82.0	448	8	ABR55871	Abr55871 Human imm
24	503.5	82.0	449	2	AAR43339	Aar43339 Completel
25	503.5	82.0	449	2	AAW49816	Aaw49816 Amino aci
26	502.5	81.8	164	5	ABG71534	Abg71534 Mouse ant
27	498.5	81.2	136	1	AAP70624	Aap70624 Sequence
28	498.5	81.2	136	2	AAW10239	Aaw10239 Chimeric
29	498.5	81.2	136	2	AAW10584	Aaw10584 Anti-hepa
30	498.5	81.2	136	2	AAW16340	Aaw16340 Mouse-hum
31	498.5	81.2	136	2	AAW41054	Aaw41054 Human ant
32	498.5	81.2	136	2	AAW47510	Aaw47510 Human ant
33	498.5	81.2	136	2	AAW47517	Aaw47517 Human ant
34	498.5	81.2	136	2	AAW89535	Aaw89535 Chimeric
35	498.5	81.2	136	4	AAB98085	Aab98085 Chimeric
36	498.5	81.2	136	2	ADC65003	Adc65003 Human imm
37	497.5	81.0	117	2	AAR88716	Aar88716 Mouse ant
38	497.5	81.0	166	5	ABG71536	Abg71536 Mouse ant
39	497.5	81.0	574	7	ADE52216	Ade52216 E3Bi prot
40	497.5	81.0	2606	7	ADE52217	Ade52217 pG1EN-EH3
41	497.5	81.0	2606	7	ADE52214	Ade52214 pG1EN-EH3
42	492	80.1	272	2	AAW00557	Aaw00557 Nematode
43	492	80.1	272	2	AAW43913	Aaw43913 Mus muscu
44	490.5	79.9	119	2	AAW01585	Aaw01585 Lead bind
45	490.5	79.9	121	2	AAW00833	Aaw00833 Variable

ALIGNMENTS

```
RESULT 1
AAB10443
ID   AAB10443 standard; protein; 116 AA.
XX
AC   AAB10443;
XX
DT   01-DEC-2000  (first entry)
XX
DE   Murine monoclonal antibody MAK HE2 variable region heavy chain.
XX
KW   Murine; monoclonal antibody; MAK HE2; heavy chain; variable region;
KW   human cellular membrane antigen; tumor associated antigen; TAA; vaccine;
KW   cancer.
XX
OS   Mus sp.
XX
PN   WO200041722-A1.
XX
PD   20-JUL-2000.
XX
PF   12-JAN-2000; 2000WO-EP000174.
XX
PR   13-JAN-1999;   99CH-00000051.
XX
PA   (IGEN-) IGENEON GMBH.
XX
PI   Eckert H, Loibner H;
XX
DR   WPI; 2000-475956/41.
XX
PT   Novel use of antibodies against human cellular membrane antigens for
PT   vaccination against cancer.
XX
PS   Example 3; Page 47; 54pp; German.
XX
CC   This invention describes the novel use of an antibody targeted to a human
CC   cellular membrane antigen, to manufacture a medicament to
CC   prophylactically and/or therapeutically vaccinate against cancer. The
CC   antibodies against tumor associated antigen (TAA) for prophylactic and/or
CC   therapeutic vaccination against cancer may be used in low doses (when
CC   compared to antibodies against TAA for passive immunotherapy), typically
CC   less than 1 mg by injection. The antibodies also have a long continual
CC   activity that directly induces immunity and their shelf life is unlimited
CC   (fresh vaccination is always possible). This sequence represents the
CC   murine monoclonal antibody MAK HE2 variable region heavy chain fragment
CC   which is used in the method of the invention
XX
SQ   Sequence 116 AA;
```

```
Query Match     100.0%;    Score 614;  DB 3;  Length 116;
Best Local Similarity  100.0%;  Pred. No. 8e-47;
Matches 116;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60

Qy     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116

RESULT 2
AAW49814
ID  AAW49814 standard; protein; 119 AA.
XX
AC  AAW49814;
XX
DT  25-MAR-2003  (revised)
DT  24-SEP-1998  (first entry)
XX
DE  Amino acid sequence of the mouse antibody C4G1 mature heavy chain.
XX
KW  Heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody;
KW  inhibition; antigen; cardiovascular disease; thromboembolic disorder;
KW  cancer; acute myocardial infarction; unstable angina; stroke;
KW  transient ischemic episode; pulmonary embolism; deep vein thrombosis;
KW  extracorporeal cardiopulmonary circulation.
XX
OS  Mus sp.
XX
XX
FH                  Key            Location/Qualifiers
FT                  Domain         31..35
FT                                 /note= "complementarity determining region"
FT                  Domain         50..66
FT                                 /note= "complementarity determining region"
FT                  Domain         99..108
FT                                 /note= "complementarity determining region"
XX
PN  US5777085-A.
XX
PD  07-JUL-1998.
XX
PF  17-MAY-1995;  95US-00458516.
XX
PR  20-DEC-1991;  91US-00812111.
PR  09-JUN-1992;  92US-00895952.
PR  11-SEP-1992;  92US-00944159.
PR  03-MAY-1993;  93US-00059159.
XX
PA  (PROT-) PROTEIN DESIGN LABS INC.
PA  (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
PI  Tso JY,  Co MS;
XX
DR  WPI; 1998-398136/34.
XX
PT  New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse
PT  C4G1 antibody, used for inhibiting platelet aggregation for treating
PT  cardiovascular and thromboembolic disorders.
XX
PS  Claim 1; Fig 5B; 35pp; English.
XX
CC  This is the amino acid sequence of the humanised antibody C4G1 heavy
CC  chain, used in the method of the invention involving the creation of a
CC  humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody. The
CC  humanised Ig is capable of binding to GPIIb/IIIa and inhibiting platelet
CC  aggregation and also the releasing reaction of platelets. The Ig can be
CC  used for treating cardiovascular diseases and thromboembolic disorders,
CC  e.g. acute myocardial infarction, unstable angina, stroke, transient
CC  ischemic episodes, deep vein thrombosis and pulmonary embolism,
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CC  extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC  diagnosing the presence and location of a thrombus, or certain types of
CC  cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC  detection of GPIIb/IIIa antigens or for isolating platelets. (Updated on
CC  25-MAR-2003 to correct PA field.)
XX
SQ  Sequence 119 AA;

Query Match     90.3%;    Score 554.5;  DB 2;  Length 119;
Best Local Similarity  91.6%;  Pred. No. 1.5e-41;
Matches 109;  Conservative  3;  Mismatches  4;  Indels  3;  Gaps  2;

Qy      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||||||||||:|||||:||||||||||||||||||||||||||||||||||:||||||
Db      1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 60

Qy     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
          ||||||||||| :||||:||||||||||||||||||: :||   ||||||:|||||||
Db     61 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 119

RESULT 3
ABR55869
ID  ABR55869 standard; protein; 119 AA.
XX
AC  ABR55869;
XX
DT  02-SEP-2003  (first entry)
XX
DE  Anti-glycoprotein IIb/IIIa MAb mature heavy chain variable region.
XX
KW  Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
KW  glycoprotein IIb/IIIa; monoclonal antibody; human; antibody.
XX
OS  Mus musculus.
XX
PN  WO2003031464-A2.
XX
PD  17-APR-2003.
XX
PF  09-OCT-2002;  2002WO-US032263.
XX
PR  10-OCT-2001;  2001US-0328523P.
PR  19-OCT-2001;  2001US-0344692P.
PR  28-NOV-2001;  2001US-0334233P.
PR  28-NOV-2001;  2001US-0334301P.
PR  07-JUN-2002;  2002US-0387292P.
PR  25-JUN-2002;  2002US-0391777P.
PR  17-JUL-2002;  2002US-0396594P.
PR  16-AUG-2002;  2002US-0404249P.
PR  28-AUG-2002;  2002US-0407527P.
XX
PA  (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI  De Frees S,  Zopf D,  Bayer R,  Bowe C,  Hakes D,  Chen X;
XX
DR  WPI; 2003-449162/42.
XX
PT  Remodeling a peptide, by removing a saccharyl subunit from the peptide to
PT  form truncated glycan, and adding or deleting glycosyl groups to a
PT  peptide and/or adding modifying group of a peptide to remodel the
PT  peptide.
XX
PS  Example; Fig 77; 900pp; English.
XX
CC  The invention relates to a cell-free, in vitro method of remodeling a
CC  peptide. The method involves removing a saccharyl subunit from the
CC  peptide, thus forming a truncated glycan, and contacting the truncated
CC  glycan with at least one glycosyltransferase and at least one glycosyl
CC  donor under conditions suitable to transfer at least one glycosyl donor
CC  to the truncated glycan, thus remodeling the peptide. Conjugates can be
CC  formed between a granulocyte colony stimulating factor (G-CSF) peptide,
CC  interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
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CC   Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
CC   (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
CC   peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
CC   peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
CC   peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
CC   receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
CC   glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti HER2
CC   antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
CC   CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,
CC   insulin peptide, hepatitis B surface antigen (HbsAg), human growth
CC   hormone (HGH) peptide, and a modifying group, where the modifying group
CC   is covalently attached to the peptide through an intact glycosyl linking
CC   group. The method is useful for a cell-free, in vitro method of
CC   remodeling the above mentioned peptides. The present sequence represents
CC   an anti-glycoprotein IIb/IIIa monoclonal antibody mature heavy chain
CC   variable region
XX
SQ   Sequence 119 AA;

Query Match   90.3%; Score 554.5; DB 6; Length 119;
Best Local Similarity   91.6%; Pred. No. 1.5e-41;
Matches 109; Conservative   3; Mismatches   4; Indels   3; Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
             ||||||||||||:||||||:|||||||||||||||||||||||||||||||||:|||||||
Db   1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
             ||||||||||| ||||:||||||||||||||||||| ||| |||||||:||||||||
Db   61 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 119

RESULT 4
AAR39266
ID   AAR39266 standard; protein; 138 AA.
XX
AC   AAR39266;
XX
DT   25-MAR-2003 (revised)
DT   29-NOV-1993 (first entry)
XX
DE   Mouse C4G1 Ig heavy-chain.
XX
KW   Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIa/IIIb;
KW   monoclonal antibody; platelet agglutination; humanised antibody.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..20
FT   /label= signal_peptide
FT   Protein   21..138
FT   /label= light_chain
FT   Region   50..54
FT   /label= complementarity_determining_region_1
FT   Region   69..85
FT   /label= CDR_2
FT   Region   118..127
FT   /label= CDR_3
XX
PN   WO9311133-A1.
XX
PD   08-JUL-1993.
XX
PF   15-DEC-1992; 92WO-JP001630.
XX
PR   20-DEC-1991; 91US-00812111.
PR   09-JUN-1992; 92US-00895952.
PR   11-SEP-1992; 92US-00944159.
XX
PA   (YAMA) YAMANOUCHI PHARM CO LTD.
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX

PI   Co MS, Tso JY;
XX
DR   WPI; 1993-227275/28.
DR   N-PSDB; AAQ45663.
XX
PT   Compsn. contg. immunoglobulin specific for the GP-IIB and -IIIA protein -
PT   for treating disorders related to vascular thrombosis.
XX
PS   Disclosure; Fig 2B; 54pp; Japanese.
XX
CC   This is the sequence of the mouse C4G1 immunoglobulin heavy chain. See
CC   AAR39265 for the light chain sequence. The antibody is specific for the
CC   GPIIa/IIIb protein and inhibits platelet agglutination. The Ig is thus
CC   useful in the treatment of thrombosis. (Updated on 25-MAR-2003 to correct
CC   PN field.)
XX
SQ   Sequence 138 AA;

Query Match   90.3%; Score 554.5; DB 2; Length 138;
Best Local Similarity   91.6%; Pred. No. 1.8e-41;
Matches 109; Conservative   3; Mismatches   4; Indels   3; Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
             ||||||||||||:||||||:|||||||||||||||||||||||||||||||||:|||||||
Db   20 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
             ||||||||||| ||||:||||||||||||||||||| ||| |||||||:||||||||
Db   80 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 138

RESULT 5
AAW49810
ID   AAW49810 standard; protein; 138 AA.
XX
AC   AAW49810;
XX
DT   25-MAR-2003 (revised)
DT   24-SEP-1998 (first entry)
XX
DE   Variable region of mouse antibody C4G1 light chain.
XX
KW   Mouse; antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;
KW   inhibition; antigen; cardiovascular disease; thromboembolic disorder;
KW   cancer; acute myocardial infarction; unstable angina; stroke;
KW   transient ischemic episode; pulmonary embolism; deep vein thrombosis;
KW   extracorporeal cardiopulmonary circulation.
XX
OS   Mus sp.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..19
FT   Protein   20..138
FT   /note="mature protein"
FT   Domain   50..54
FT   /note="complementarity determining region"
FT   Domain   69..85
FT   /note="complementarity determining region"
FT   Domain   118..127
FT   /note="complementarity determining region"
XX
PN   US5777085-A.
XX
PD   07-JUL-1998.
XX
PF   17-MAY-1995; 95US-00458516.
XX
PR   20-DEC-1991; 91US-00812111.
PR   09-JUN-1992; 92US-00895952.
PR   11-SEP-1992; 92US-00944159.
PR   03-MAY-1993; 93US-00059159.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX

PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Tso JY, Co MS;
XX
DR WPI; 1998-398136/34.
DR N-PSDB; AAV36742.
XX
PT New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse
PT C4G1 antibody, used for inhibiting platelet aggregation for treating
PT cardiovascular and thromboembolic disorders.
XX
PS Disclosure; Fig 2B; 35pp; English.
XX
CC This is the amino acid sequence of the mouse antibody C4G1 heavy chain,
CC used in the method of the invention involving the creation of a humanised
CC immunoglobulin (Ig) derived from the mouse C4G1 antibody. The humanised
CC Ig is capable of binding to GPIIb/IIIa and inhibiting platelet
CC aggregation and also the releasing reaction of platelets. The Ig can be
CC used for treating cardiovascular diseases and thromboembolic disorders,
CC e.g. acute myocardial infarction, unstable angina, stroke, transient
CC ischemic episodes, deep vein thrombosis and pulmonary embolism,
CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC diagnosing the presence and location of a thrombus, or certain types of
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC detection of GPIIb/IIIa antigens or for isolating platelets. (Updated on
CC 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 138 AA;

Query Match   90.3%;   Score 554.5; DB 2;   Length 138;
Best Local Similarity   91.6%;   Pred. No. 1.8e-41;
Matches   109; Conservative   3; Mismatches   4; Indels   3; Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        ||||||||||||| |||| ||||||||||||||||||||||||||||||| |||||||||
Db 20 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 79

Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
        |||||||||||| ||| |||||||||||||||||||| || |||||| ||||||||
Db 80 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 138

RESULT 6
AAW01580
ID AAW01580 standard; protein; 119 AA.
XX
AC AAW01580;
XX
DT 22-AUG-1997 (first entry)
XX
DE Lead binding MAb 14F11 heavy chain variable region.
XX
KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal.
XX
OS Mus musculus.
XX
PN WO9639518-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US009258.
XX
PR 05-JUN-1995; 95US-00462798.
PR 10-OCT-1995; 95US-00541373.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Wylie DB, Lopez O, Murray PJ;
XX
DR WPI; 1997-043140/04.
DR N-PSDB; AAT58254.
XX

XX
PT DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as lead
PT cations.
XX
PS Claim 12; Page 63; 125pp; English.
XX
CC The present sequence represents the heavy chain variable region for
CC monoclonal antibody (MAb) 14F11, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from mouse hybridoma cells.
CC The protein can be used for binding heavy metals, such as lead cations.
CC It can be used for detecting, removing, adding or neutralising the heavy
CC metals in biological and inanimate systems. It can be used in e.g.
CC aqueous liquid systems, in biological or environmental systems or in such
CC compositions as perfumes, cosmetics, pharmaceuticals, health care
CC products, skin treatment products, pesticides, herbicides, solvents used
CC in the production of semi-conductor and integrated circuit components and
CC production materials for electronic components. The products can provide
CC for applications involving minute amounts of specific heavy metals
XX
SQ Sequence 119 AA;

Query Match   89.0%;   Score 546.5; DB 2;   Length 119;
Best Local Similarity   89.9%;   Pred. No. 7.7e-41;
Matches   107; Conservative   3; Mismatches   6; Indels   3; Gaps   1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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Db   1 EVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYPCARDGP---WFAYWGQGTLVTVSA 116
        |||||||||||||||||||||||||||||||||||| ||| :||||||||||||||
Db 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARSGYGHWYFDVWGAGTTVTVSS 119

RESULT 7
AAE34367
ID AAE34367 standard; protein; 138 AA.
XX
AC AAE34367;
XX
DT 14-MAY-2003 (first entry)
XX
DE Escherichia coli heavy chain variable region.
XX
KW S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;
KW hepatotropic.
XX
OS Escherichia coli.
XX
FH Key   Location/Qualifiers
FT Region   31..35
FT   /note= "CDR1"
FT Region   50..66
FT   /note= "CDR2"
FT Region   99..111
FT   /note= "CDR3"
XX
PN WO200292819-A1.
XX
PD 21-NOV-2002.
XX
PF 15-MAY-2002; 2002WO-KR000905.
XX
PR 16-MAY-2001; 2001KR-00026634.
XX
PA (YUHA-) YUHAN CORP.
XX
PI Lee JW, Ko IY, Kang HK, Song MY, Song TH, Kim CS;
XX
DR WPI; 2003-140281/13.
DR N-PSDB; AAD52608.
XX

PT   New light and heavy chain variable regions of a monoclonal antibody
PT   against the S-surface antigen of the hepatitis B virus (HBV), useful for
PT   neutralizing or removing HBV, or for preventing or treating HBV
PT   infection.
XX
PS   Claim 12; Page 17; 20pp; English.
XX
CC   The invention relates to light and heavy chain variable regions of a
CC   monoclonal antibody against S-surface antigen of the hepatitis B virus
CC   (HBV). The variable regions of the antibodies are useful against HBV S-
CC   surface antigens, e.g. adr, adw, ayr or ayw, particularly for
CC   neutralising or removing HBV. They may also be employed to treat or
CC   prevent HBV infection. The present sequence is Escherichia coli heavy
CC   chain variable region
XX
SQ   Sequence 138 AA;

Query Match   84.5%;   Score 519; DB 6;   Length 138;
Best Local Similarity   83.6%;   Pred. No. 2.4e-38;
Matches 102; Conservative   5; Mismatches   9; Indels   6; Gaps   1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          |||||||| ||||||||||||||||||| |||| ||||||||||| |||||||||||||
Db   1 QVQLQQSGTEMVRPGTSVKVSCKASGYPFTNHLIEWVKQRPGQGPEWIGVINPGSGGTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA------RDGPWFAYWGQGTLVTV 114
          |||||||||||||||||||||||| ||||||||||| ||| ||||||||| ||
Db   61 NEKFKGKATLTADKSSSTAYMQLNSLTSDDSAVYFCAIMTTFLGEGYAMDYWGQGTSVTV 120

Qy 115 SA 116
          |:
Db 121 SS 122

RESULT 8
ABG71533
ID   ABG71533 standard; protein; 164 AA.
XX
AC   ABG71533;
XX
DT   31-DEC-2002 (first entry)
XX
DE   Mouse anti-acetyllysine monoclonal antibody (mAb) heavy chain #1.
XX
KW   Mouse; anti-acetyllysine monoclonal antibody; N epsilon-acetyllysine;
KW   functional analysis; acetyllysine-containing protein; pathosis;
KW   acetylated protein; disease diagnosis; histone acetylation; mAb;
KW   antibody-producing immortalised cell; heavy chain.
XX
OS   Mus sp.
XX
PN   WO20027496 2-A1.
XX
PD   26-SEP-2002.
XX
PF   13-MAR-2002; 2002WO-JP002330.
XX
PR   15-MAR-2001; 2001JP-00074263.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA   (NIHA) JAPAN ENERGY CORP.
XX
PI   Komatsu Y, Yoshida M;
XX
DR   WPI; 2002-750555/81.
DR   N-PSDB; ABS55467.
XX
PT   Production of anti-acetyllysine monoclonal antibody capable of
PT   recognising Napproximatelyi-acetyllysine regardless of types of adjacent
PT   amino acids, useful in e.g. disease diagnosis and searching for novel
PT   acetyllysine-containing proteins.
XX
PS   Example 4; Fig 4; 45pp; Japanese.

CC   The present invention relates to a mouse anti-acetyllysine monoclonal
CC   antibody (mAb) capable of recognising N epsilon-acetyllysine, and a
CC   method for produced the monoclonal antibody. The produced antibody is
CC   useful in searching for and functional analysis of novel acetyllysine-
CC   containing proteins, disease diagnosis, particularly in studying pathosis due to acetylated
CC   proteins, disease diagnosis, facilitating detection of variation in
CC   acetylation levels of histone influenced by various stimulations during
CC   Western blotting, analysis of the variable region in the DNA sequence of
CC   an antibody gene of an antibody-producing immortalised cell, and judging
CC   the degree of homology specific to the sequence during the protein
CC   translation. The monoclonal antibody of the invention is capable of
CC   recognising N epsilon-acetyllysine regardless of the type of adjacent
CC   amino acids and accepting adjacent amino acids over a broad range. The
CC   present sequence represents a heavy chain of mouse anti-acetyllysine mAb.
XX
SQ   Sequence 164 AA;

Query Match   84.3%;   Score 517.5; DB 5;   Length 164;
Best Local Similarity   84.0%;   Pred. No. 4e-38;
Matches 100; Conservative   6; Mismatches   10; Indels   3; Gaps   1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          |||||||||||||||||| ||||||| ||||| ||||||||| |||||||| |||||||
Db   1 QVQLQQSGAELVRPGTSVKMSCKAAGYTFTNHWIGWVKQRPGHGLEWIGDIYPGSGYTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFAYWGQGTLVTVSA 116
          ||||||||||||| ::|||||||:::||| |:::| ||||||||||||||
Db   61 NEKFKGKATLTADTSSTAYMQLSSLTSEDSAIYYCARSDYYGSWFAYWGQGTLVTVSA 119

RESULT 9
AAR12360
ID   AAR12360 standard; protein; 137 AA.
XX
AC   AAR12360;
XX
DT   25-MAR-2003 (revised)
DT   15-AUG-1991 (first entry)
XX
DE   Heavy chain variable region of murine 4D12 immunoglobulin.
XX
KW   Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
OS   Mus musculus.
XX
PN   WO9107493-A.
XX
PD   30-MAY-1991.
XX
PF   13-NOV-1989;   89US-00433730.
XX
PR   13-NOV-1989;   89US-00433730.
XX
PA   (XOMA) XOMA CORP.
PA   (GREC) GREEN CROSS CORP.
XX
PI   Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
XX
DR   WPI; 1991-178105/24.
DR   N-PSDB; AAQ12062.
XX
PT   New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT   -1 antigen from sample.
XX
PS   Disclosure; Fig 17; 107pp; English.
XX
CC   This is the heavy - chain variable (V) region of a mouse monoclonal
CC   antibody (MAb), 4D12, and is specific for an HIV-1 viral antigen. It is
CC   used in the construction of a chimeric MAb comprising heavy and light
CC   chains having murine V regions and human C regions. The chimeric MAbs are
CC   more effective than murine MAb 4D12 since they have an increased
CC   compatibility in humans. The heavy and light chain V-regions are joined

```
CC   by manipulating their respective joining (J) regions, to generate
CC   restriction enzyme recognition sites. The chimeric MAbs can be used as
CC   immunoconjugates, in association with e.g. toxins for HIV treatment. They
CC   can also be used in diagnosis of HIV. See also AAQ12056-61 and AAQ12063.
CC   (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC   correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
XX
SQ   Sequence 137 AA;

Query Match           83.9%;  Score 515;  DB 2;  Length 137;
Best Local Similarity 84.7%;  Pred. No. 5.5e-38;
Matches 100;  Conservative  4;  Mismatches 12;  Indels 2;  Gaps 1;

Qy       1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
           |||:|||||:|||||:||||||:|||||||||||||||||||||||||||||||||||||
Db      20 QVHLQQSGAEMVRPGISVKVSCRASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTTY 79

Qy      61 NEKFKGKATLTADKSSSTAYMQLSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
           |||:||||||||||||| |:|||:|||||||||||| :: ||   ||||||| ||||:
Db      80 NEKFKDKTTMTADKSSSTAYMHLDSLTSDDSAVYLCARTGSGHALEYWGQGTSVTVSS 137


RESULT 10
AAR12238
ID   AAR12238 standard; protein; 137 AA.
XX
AC   AAR12238;
XX
DT   25-MAR-2003 (revised)
DT   19-AUG-1991 (first entry)
XX
DE   Mouse MAb 4D12 H chain V region.
XX
KW   HIV-1; chimera.
XX
OS   Mus sp.
XX
PN   WO9107494-A.
XX
PD   30-MAY-1991.
XX
PF   13-NOV-1989;   89US-00433703.
XX
PR   13-NOV-1989;   89US-00433703.
XX
PA   (XOMA ) XOMA CORP.
PA   (GREC ) GREEN CROSS CORP.
PA   (ZOMA-) ZOMA CORP.
XX
PI   Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
XX
DR   WPI; 1991-178106/24.
DR   N-PSDB; AAQ12018.
XX
PT   New chimeric mouse human antibodies - used in treatment, diagnosis and
PT   prophylaxis of HIV infections.
XX
PS   Disclosure; Fig 17; 108pp; English.
XX
CC   The mouse VH gene product may be used to produce chimeric mouse- human
CC   Abs against HIV-1 comprising human Ig constant regions and murine
CC   variable regions. These novel sequence are useful in treatment, diagnosis
CC   and prophylaxis of HIV infections, and may be produced by a bacterial,
CC   yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
CC   PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 137 AA;

Query Match           83.9%;  Score 515;  DB 2;  Length 137;
Best Local Similarity 84.7%;  Pred. No. 5.5e-38;
Matches 100;  Conservative  4;  Mismatches 12;  Indels 2;  Gaps 1;

Qy       1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
```

```
Db      20 QVHLQQSGAEMVRPGTSVKVSCRASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTTY 79

Qy      61 NEKFKGKATLTADKSSSTAYMQLSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
Db      80 NEKFKDKTTMTADKSSSTAYMHLDSLTSDDSAVYLCARTGSGHALEYWGQGTSVTVSS 137


RESULT 11
AAR09427
ID   AAR09427 standard; protein; 141 AA.
XX
AC   AAR09427;
XX
DT   25-MAR-2003 (revised)
DT   04-MAR-1993 (first entry)
XX
DE   ME4 Heavy Chain V Region (mouse).
XX
KW   Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
KW   antigen; diagnosis; cancer; tumour.
XX
OS   Mus musculus.
XX
PN   WO9002569-A.
XX
PD   22-MAR-1990.
XX
PF   08-SEP-1988;   88US-00241744.
XX
PR   08-SEP-1988;   88US-00241744.
PR   13-SEP-1988;   88US-00243739.
PR   04-OCT-1988;   88US-00253002.
PR   19-JUN-1989;   89US-00367641.
PR   21-JUL-1989;   89US-00382768.
XX
PA   (ITGE-) INT GENETIC ENG INC.
PA   (INGE-) INGENE INT GENETIC.
XX
PI   Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX
DR   WPI; 1990-115825/15.
DR   N-PSDB; AAQ08609.
XX
PT   Chimeric mouse-human antibodies - prepd. using genes coding for constant
PT   human region murine variable region, esp. to 3 tumour antigen.
XX
PS   Claim 13; Page 123 + Fig 30; 173pp; English.
XX
CC   The sequence is used in the prodn. of a chimeric antibody mol, comprising
CC   two light chains and two heavy chains, each having a constant region
CC   (human) and a variable region (murine) having specificity to an antigen
CC   bound by murine monoclonal antibody (MAb) B38.1. The chimeric antibodies
CC   can be used for any purpose for which the original murine MAbs can be
CC   used, with the advantage that they are more compatible with the human
CC   body. They are esp. used for the diagnosis and treatment of cancer.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 141 AA;

Query Match           83.9%;  Score 515;  DB 2;  Length 141;
Best Local Similarity 85.0%;  Pred. No. 5.6e-38;
Matches 102;  Conservative  4;  Mismatches 10;  Indels 4;  Gaps 2;

Qy       1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
           ||||||||||||||||||||||::|||||||||:||:||||||||||||||||||||:  :
Db      20 QVQLQQSGAELVRPGTSVKVSCTTSGYAFTNYLMEWMKQRPGQGLEWIGVINPGSGDAKY 79

Qy      61 NEKFKGKATLTADKSSSTAYMQLSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA 116
           |:|||||||||||||| |:|||| ||||||||||||||     ||  |||||||:||||
Db      80 NENFKGKATLTADKSSTSYMQLSSLTSDDSAVYFCARGHYGGYVMDYWGQGTSVTVSA 139
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```
RESULT 12
AAW06216
ID   AAW06216 standard; protein; 141 AA.
XX
AC   AAW06216;
XX
DT   25-MAR-2003 (revised)
DT   13-FEB-1997 (first entry)
XX
DE   MAb ME4 heavy chain variable region.
XX
KW   Chimeric antibody; monoclonal antibody; ME4; antibody engineering;
KW   tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
KW   ovary carcinoma; melanoma; cancer; diagnosis; therapy; heavy chain.
XX
OS   Mus sp.
XX
PN   US5576184-A.
XX
PD   19-NOV-1996.
XX
PF   27-DEC-1994;   94US-00364001.
XX
PR   06-SEP-1988;   88US-00240624.
PR   08-SEP-1988;   88US-00241744.
PR   13-SEP-1988;   88US-00243739.
PR   04-OCT-1988;   88US-00253002.
PR   19-JUN-1989;   89US-00367641.
PR   21-JUL-1989;   89US-00382768.
PR   06-MAY-1991;   91US-00659401.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;
XX
DR   WPI; 1997-011249/01.
DR   N-PSDB; AAT43441.
XX
PT   Chimeric mouse-human antibodies - recognise a human tumour antigen, used
PT   for the treatment and diagnosis of human cancers.
XX
PS   Example 3; Fig 30; 102pp; English.
XX
CC   The heavy chain variable region (AAW06216) of mouse monoclonal antibody
CC   ME4 is the product of a cDNA clone (AAT43441) isolated from a ME4
CC   hybridoma cDNA library. MAb ME4 (IgG1) binds to an antigen that is
CC   expressed on the surface of human lung, breast, colon and ovary
CC   carcinomas and melanomas, but not on most normal adult tissues. The heavy
CC   chain and light chain variable regions (see also AAW06215) of ME4 can be
CC   linked to human constant regions and expressed in transformed host cells.
CC   Novel mouse-human chimeric antibodies (see also AAW06209-14 and AAW06217-
CC   18) can be produced that have specificity to human tumour antigens for
CC   use in the treatment and diagnosis of human cancer. (Updated on 25-MAR-
CC   2003 to correct PF field.)
XX
SQ   Sequence 141 AA;

Query Match             83.9%;  Score 515;  DB 2;  Length 141;
Best Local Similarity   85.0%;  Pred. No. 5.6e-38;
Matches  102;  Conservative    4;  Mismatches    4;  Indels   10;  Gaps     2;

Qy          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
              ||||||||||||||||||||||:|||||||||:|||||||||||||||||||||||
Db         20 QVQLQQSGAELVRPGTSVKVSCTTSGYAFTNYLMEWMKQRPGQGLEWIGVINPGSGDAKY 79

Qy         61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA 116
              ||||||||||||||||| ||||||||||||||||||  ::: ||||||||||||
Db         80 NENFKGKATLTADKSSSTSYMQLSSLTSDDSAVYFCARGHYGGYFVMDYWGQGTSVTVSA 139

RESULT 13
AAW85063
ID   AAW85063 standard; protein; 141 AA.
```

```
XX
AC   AAW85063;
XX
DT   20-MAR-2003 (revised)
DT   16-APR-1999 (first entry)
XX
DE   Mouse ME4 heavy chain variable region.
XX
KW   Heavy chain variable region; murine antibody ME4; antibody ING-1;
KW   chimeric immunoglobulin; human tumour antigen; chimeric antibody;
KW   treatment; human cancer.
XX
OS   Mus sp.
XX
PN   US5843685-A.
XX
PD   01-DEC-1998.
XX
PF   06-JUN-1995;   95US-00466034.
XX
PR   06-SEP-1988;   88US-00240624.
PR   08-SEP-1988;   88US-00241744.
PR   13-SEP-1988;   88US-00243739.
PR   04-OCT-1988;   88US-00253002.
PR   19-JUN-1989;   89US-00367641.
PR   21-JUL-1989;   89US-00382768.
PR   06-SEP-1989;   89WO-US003852.
PR   06-MAY-1991;   91US-00659401.
PR   27-DEC-1994;   94US-00364001.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Horwitz AH,  Lei S,  Chang CP,  Better MD,  Robinson RR;
XX
DR   WPI; 1999-044574/04.
DR   N-PSDB; AAV71159.
XX
PT   Chimeric antibody specific for human tumour antigen - useful as
PT   immunoassay, imaging or antitumour agent.
XX
PS   Example 3; Fig 30; 92pp; English.
XX
CC   The present sequence represents the heavy chain variable region of murine
CC   antibody ME4. The sequence was used to create chimeric mouse-human
CC   immunoglobulins which recognise the human tumour antigen bound by
CC   antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The
CC   chimeric antibodies also have an antigen-binding site that competitively
CC   inhibits the binding of antibody ING-1, and mediate complement-dependent
CC   cytolysis of target cells or antibody-dependent cellular cytotoxicity to
CC   target cells. The chimeric antibodies can be used for therapeutic
CC   purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 141 AA;

Query Match             83.9%;  Score 515;  DB 2;  Length 141;
Best Local Similarity   85.0%;  Pred. No. 5.6e-38;
Matches  102;  Conservative    4;  Mismatches    4;  Indels   10;  Gaps     2;

Qy          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
              ||||||||||||||||||||||:|||||||||:|||||||||||||||||||||||
Db         20 QVQLQQSGAELVRPGTSVKVSCTTSGYAFTNYLMEWMKQRPGQGLEWIGVINPGSGDAKY 79

Qy         61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFA--YWGQGTLVTVSA 116
              ||||||||||||||||| ||||||||||||||||||  ::: ||||||||||||
Db         80 NENFKGKATLTADKSSSTSYMQLSSLTSDDSAVYFCARGHYGGYFVMDYWGQGTSVTVSA 139

RESULT 14
ABU58897
ID   ABU58897 standard; protein; 141 AA.
XX
AC   ABU58897;
```

```
Matches  102;  Conservative    4;  Mismatches   10;  Indels   4;  Gaps    2;

Qy     1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSSGGTNY 60
         |||||||||||||||||||||:||| |||||||| |||||||||||||||||| :||||||
Db    20 QVQLQQSGAELVRPGTSVKVSCTTSGYAFTNYLMEWMKQRPGQGLEWIGVINPGSDAKY 79

Qy    61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVFCARD--GPWFA--YWGQGTLVTVSA 116
         |||||||||||||||||:|||||||||||||||||||   :|:    ||||||||||||
Db    80 NENFKGKATLTADKSSSTSYMQLSSLTSDDSAVFCARGHYGGYFVMDYWGQGTSVTVSA 139
```

```
XX
RESULT 15
AAW34515
XX
ID    AAW34515 standard; protein; 138 AA.
XX
AC    AAW34515;
XX
DT    19-MAR-1998  (first entry)
XX
DE    Variable heavy chain of antibody from hybridoma 5-465-210.
XX
KW    Variable region coding sequence; constant region epitope; hybridoma;
KW    antibody detection; antigen/antibody complex; variable heavy chain.
XX
OS    Mus musculus.
XX
PN    WO9727486-A1.
XX
PD    31-JUL-1997.
XX
PF    17-JAN-1997;  97WO-US001074.
XX
PR    23-JAN-1996;  96US-00589939.
XX
PA    (ABBO )  ABBOTT LAB.
XX
PI    Hackett JR, Hoff JA, Ostrow DH, Golden AM;
XX
DR    WPI; 1997-393833/36.
DR    N-PSDB; AAT98832.
XX
PT    Use of antibody constant region epitope(s) - as control or calibrator
PT    reagents in assays for detecting the presence of an antibody in a test
PT    sample.
XX
PS    Disclosure; Page 60; 109pp; English.
XX
CC    This sequence represents the variable heavy chain of the antibody
CC    produced by hybridoma 5-465-210, and can be detected using the method of
CC    the invention. The method is for detecting the presence of antibody which
CC    may be present in a test sample. It comprises contacting a test sample
CC    suspected of containing the antibody with an antigen specific for the
CC    antibody to allow the formation of antigen/antibody complexes; detecting
CC    the presence of the antibody which may be present in the test sample and
CC    employing, as a control or calibrator, a reagent which binds to the
CC    antigen. The improvement to this method over previous methods, comprises
CC    employing, as the control or calibrator, a reagent comprising one or more
CC    antibody constant region epitopes, where the reagent binds to the antigen
CC    and is homogeneous with respect to specificity and affinity. The method
CC    can be also be used for detecting the presence of antibodies developed
CC    against more than one antigen. The method is used particularly for the
CC    detection of human antibodies specific for a given antigen, e.g. HIV-1,
CC    hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all
CC    of the problems associated with using an immune sera in the manufacture
CC    of calibrators and positive controls. The present reagents can be readily
CC    and reproducibly generated in virtually unlimited quantities and are also
CC    useful for quantitating, and monitoring the integrity of, the antigen
CC    used in assays
XX
SQ    Sequence 138 AA;

Query Match            83.1%;  Score 510.5;  DB 2;  Length 138;
Best Local Similarity  84.9%;  Pred. No. 1.4e-37;
```

```
XX
DT    16-APR-2003  (first entry)
XX
DE    Mouse antibody heavy chain variable region #4.
XX
KW    Mouse; human tumour antigen; anti-human tumour antigen-antibody;
KW    ING-1 antibody; cell line HB9812; immunoassay; imaging; tumour diagnosis;
KW    tumour therapy; cytostatic; heavy chain variable region.
XX
OS    Mus sp.
XX
PN    US6461824-B1.
XX
PD    08-OCT-2002.
XX
PF    06-JUN-1995;  95US-00467142.
XX
PR    06-SEP-1988;  88US-00240624.
PR    08-SEP-1988;  88US-00241744.
PR    13-SEP-1988;  88US-00243739.
PR    04-OCT-1988;  88US-00253002.
PR    19-JUN-1989;  89US-00367641.
PR    21-JUL-1989;  89US-00382768.
PR    06-SEP-1989;  89WO-US003852.
PR    06-MAY-1991;  91US-00659401.
PR    27-DEC-1994;  94US-00364001.
XX
PA    (XOMA )  XOMA TECHNOLOGY LTD.
XX
PI    Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX
DR    WPI; 2003-196707/19.
DR    N-PSDB; ABK79242.
XX
PT    Antibody for detecting antigen in animal or killing cells carrying
PT    antigen comprises human constant region and variable region having
PT    specificity for human tumor antigen bound by ING-1 antibody.
XX
PS    Example 3; Fig 30; 101pp; English.
XX
CC    The invention describes an antibody comprising a human constant region
CC    and a variable region having specificity for the human tumour antigen
CC    bound by the ING-1 antibody, where the ING-1 is produced by cell line
CC    HB9812 as deposited with ATCC, and the antibody has the same affinity as
CC    the ING-1 for the human tumour antigen. The antibody is useful in an
CC    immunoassay method for detecting an antigen in a sample by contacting a
CC    label-detectable antigen in the sample with the presence of the antibody; for
CC    use in an imaging method for revealing the presence of a label-detectable
CC    antigen in an animal by contacting the antibody with a part of the animal
CC    suspected of containing the antigen, detecting the label and relating the
CC    detected label to the presence of the antigen; and for killing cells
CC    carrying an antigen by contacting the cells with the antibody and
CC    allowing the killing to occur. The antibodies are useful in tumour
CC    diagnosis and therapy. The chimeric antibodies bind to the surface of
CC    human tumour cells but do not bind detectably to normal cells, e.g.,
CC    fibroblasts, endothelial cells or epithelial cells in the major organs.
CC    The high biological activity of the chimeric antibodies against human
CC    tumour cell lines combined with minimal reactivity with normal tissues
CC    imply that these antibodies may mediate selective destruction of
CC    malignant tissue. The presence of human antibodies rather than murine antigenic
CC    determinants on the chimeric antibodies increases their resistance to
CC    rapid clearance from the body relative to the original murine mAbs. This
CC    resistance to clearance enhances the potential utility of these chimeric
CC    antibodies, as well as their derivatives, in tumour diagnosis and
CC    therapy. This is the amino acid sequence of a mouse antibody heavy chain
CC    variable region used in the creation of an anti-human tumour antigen-
CC    antibody
XX
SQ    Sequence 141 AA;

Query Match            83.9%;  Score 515;  DB 6;  Length 141;
Best Local Similarity  85.0%;  Pred. No. 5.6e-38;
```

Matches 101; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

```
Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
         ||||||||||||||||||||||||||||||||||||| :||||||||||||||| |  |
Db  20 QVHLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVTQRPGQGLEWIGVINPGSDFTYY 79

Qy  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR---DGPWFAYWGQGTLVTVSA 116
         ||||||:||||||||||||||||| :||||||||||||   :| ||||| :|||
Db  80 NEKFKGRATLTADKSSSTAYMQLISLTSDDSAVYFCARTIVTTDYFDYWGQGTPLTVSS 138
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Search completed: August 16, 2004, 11:12:17
Job time : 51.4574 secs

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              GenCore version 5.1.6
OM protein - protein search, using sw model
              Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:    August 16, 2004, 11:08:06 ; Search time 46.5426 Seconds
                                       (without alignments)
                                       649.568 Million cell updates/sec

Title:         US-09-889-300A-2
Perfect score: 562
Sequence:      1 NIVMTQSPKSMSMSVGERVT.........CGQGYSYPYTFGGGTKLEIK 107

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:    1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  A_Geneseq_29Jan04.*
            1: -geneseqp1980s:*
            2: -geneseqp1990s:*
            3: -geneseqp2000s:*
            4: -geneseqp2001s:*
            5: -geneseqp2002s:*
            6: -geneseqp2003as:*
            7: -geneseqp2003bs:*
            8: -geneseqp2004s:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	* Match	Query Length	DB	ID	Description
1	562	100.0	107	2	AAW47086	Aaw47086 Mouse J59
2	562	100.0	107	2	AAY90374	Aay90374 J591 mono
3	562	100.0	107	2	AAB36225	Aab36225 Monoclona
4	562	100.0	107	3	AAB10444	Aab10444 Murine mo
5	562	100.0	109	2	AAR27144	Aar27144 1E6 kappa
6	562	100.0	121	2	AAW47085	Aaw47085 Mouse J59
7	562	100.0	121	2	AAY90370	Aay90370 J591 mono
8	562	100.0	121	2	AAB36222	Aab36222 Murine mo
9	562	100.0	127	2	AAW01145	Aaw01145 MAb 10.1
10	562	100.0	132	6	ABG74248	Abg74248 Mouse ant
11	562	100.0	135	7	ABR82783	Abr82783 Hybridoma
12	562	100.0	135	7	ABR82893	Abr82893 Hybridoma
13	534	95.0	101	5	ABB07176	Abb07176 Mouse 09
14	527	93.8	136	3	AAW01632	Aaw01632 Ber-H2 he
15	527	92.7	127	3	AAY71545	Aay71545 Mouse AF2
16	521	92.7	136	4	AAB69693	Aab69693 Murine AF
17	509	90.6	108	2	AAW00828	Aaw00828 Variable
18	503	89.5	107	6	ABO10727	Abo10727 Variable
19	503	89.5	107	6	ABR44618	Abr44618 Murine J4
20	503	89.5	107	6	ABR44671	Abr44671 Murine J4
21	490	87.2	107	6	ABO10737	Abo10737 Variable
22	490	87.2	107	6	ABO10738	Abo10738 Variable
23	490	87.2	107	6	ABR44682	Abr44682 Murine J4
24	490	87.2	107	6	ABR44624	Abr44624 Murine J4
25	490	87.2	107	6	ABR44622	Abr44622 Murine J4
26	490	87.2	107	6	ABR44681	Abr44681 Murine J4
27	487	86.7	107	6	ABO10739	Abo10739 Variable
28	487	86.7	107	6	ABR44625	Abr44625 Murine J4
29	487	86.7	107	6	ABR44683	Abr44683 Murine J4
30	485	86.3	107	6	ABO10736	Abo10736 Variable
31	485	86.3	107	6	ABR44680	Abr44680 Murine J4
32	485	86.3	107	6	ABR44621	Abr44621 Murine J4
33	484	86.1	107	6	ABO10741	Abo10741 Consensus
34	484	86.1	107	6	ABO10729	Abo10729 Variable
35	484	86.1	107	6	ABO10740	Abo10740 Variable
36	484	86.1	107	6	ABR44684	Abr44684 Murine J4
37	484	86.1	107	6	ABR44623	Abr44623 Murine J4
38	484	86.1	107	6	ABR44626	Abr44626 Murine J4
39	484	86.1	107	6	ABR44685	Abr44685 Murine J4
40	484	86.1	107	6	ABR44617	Abr44617 Murine J4
41	484	86.1	107	6	ABR44673	Abr44673 Murine J4
42	482	85.8	239	2	AAR64812	Aar64812 ScFv anti
43	478	85.1	107	6	ABO10735	Abo10735 Variable
44	478	85.1	107	6	ABR44620	Abr44620 Murine J4
45	478	85.1	107	6	ABR44679	Abr44679 Murine J4

ALIGNMENTS

```
RESULT 1
AAW47086
ID   AAW47086 standard; protein; 107 AA.
XX
AC   AAW47086;
XX
DT   26-JUN-1998  (first entry)
XX
DE   Mouse J591 monoclonal antibody light chain variable region.
XX
KW   Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
KW   cancer; vascular endothelial cell; metastatic adenocarcinoma.
XX
OS   Mus sp.
XX
PN   WO9803873-A1.
XX
PD   29-JAN-1998.
XX
PF   17-JUL-1997;   97WO-US012035.
XX
PR   18-JUL-1996;   96US-0022125P.
PR   09-APR-1997;   97US-0083B682.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Bander NH;
XX
DR   WPI; 1998-120937/11.
DR   N-PSDB; AAV13952.
XX
PT   Destroying cancer cells with agent that binds to prostate specific
PT   membrane antigen - on vascular endothelial cells near the cancer, or on
PT   normal, hypertrophic or cancerous prostatic cells, also used for
PT   diagnosis.
XX
PS   Example 12; Page 60; 94pp; English.
XX
CC   The present sequence represents the mouse J591 monoclonal antibody light
CC   chain variable region from an example of the present invention. The
CC   present invention describes the elimination of cancer cells by treating
CC   vascular endothelial cells (VEC) close to the cancer with an agent (A)
CC   able to bind to the extracellular domain (ECD) of prostate specific
CC   membrane antigen (PSMA). (A) both binds to the VEC and destroys the
CC   cancer cells. Also described are: (1) the detection of cancer tissue by
CC   detecting binding of labelled (A) to VEC close to, or within, a cancer
CC   tissue; (2) eliminating or detecting normal, benignly hyperplastic or
CC   cancerous prostate epithelial cells using optionally labelled (A); (3)
```

CC   hybridomas that produce a monoclonal antibody (MAb) that binds to PSMA.
CC   The method is used to treat renal, urothelial, colon, lung, rectal or
CC   breast cancers and metastatic adenocarcinoma of the liver. The diagnostic
CC   method is particularly used to detect recurrence of prostatic disease or
CC   to monitor the effect of treatments for prostate cancer (presence of PSMA
CC   in the serum indicates that prostate cells are being lysed). (A) binds to
CC   an epitope of PSMA expressed on live cells (contrast antibody 7E11 which
CC   only binds after cell lysis), allowing targeting of live, unfixed cells
CC   and thus providing more efficient treatment and diagnosis. Both cancer
CC   cells themselves and the VEC on which they depend are killed. All VEC
CC   close to cancer cells express PSMA, whatever the type of cancer, but
CC   normal VEC do not
XX
SQ   Sequence 107 AA;

Query Match   100.0%; Score 562; DB 2; Length 107;
Best Local Similarity   100.0%; Pred. No. 4.1e-39;
Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

RESULT 2
AAY90374
ID   AAY90374 standard; protein; 107 AA.
XX
AC   AAY90374;
XX
DT   15-JAN-2001 (first entry)
XX
DE   J591 monoclonal antibody light chain protein sequence fragment.
XX
KW   J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
KW   prostate specific membrane antigen; prostate cancer; light chain.
XX
OS   Homo sapiens.
XX
PN   US6107090-A.
XX
PD   22-AUG-2000.
XX
PF   09-APR-1997;   97US-00838682.
XX
PR   06-MAY-1996;   96US-0016976P.
PR   18-JUL-1996;   96US-0022125P.
XX
PA   (CORR) CORNELL RES FOUND INC.
XX
PI   Bander NH;
XX
DR   WPI; 1998-120937/11.
DR   N-PSDB; AAA37834.
XX
PT   Destroying cancer cells with agent that binds to prostate specific
PT   membrane antigen - on vascular endothelial cells near the cancer, or on
PT   normal, hypertrophic or cancerous prostatic cells, also used for
PT   diagnosis.
XX
PS   Example 12; Col 22; 33pp; English.
XX
CC   This sequence is a fragment of the light chain of the monoclonal antibody
CC   J591. The invention relates to an isolated antibody or its antigen
CC   binding portion (I) which binds to an extracellular domain of prostate
CC   specific membrane antigen and which does not require cell lysis to bind
CC   to the extracellular domain. The antibody or its antigen binding portion
CC   is selected for its ability to bind to live cells. (II) is useful for
CC   diagnosis of diseases associated with the presence of normal, benign

CC   hyperplastic, and cancerous epithelial cells or portions. Also it can be
CC   used for identifying the recurrence of such diseases, particularly when
CC   the disease is localised in a particular biological material of the
CC   patient for e.g. recurrence of prostatic disease. They can also be used
CC   alone or bound to a substance effective to kill cancerous prostate
CC   epithelial cells as a therapy for prostate cancer. Binding and
CC   internalising of the antibody with the prostate specific membrane
CC   antigen, permits the therapeutic use of intracellularly acting cytotoxic
CC   agents. (I) targets only prostate epithelial cells and other tissue are
CC   spared which provides safer treatment particularly for elderly patients.
CC   The antibodies bind to living prostate cells and treatments using these
CC   antibodies are more effective than those which target lysed prostate
CC   cells
XX
SQ   Sequence 107 AA;

Query Match   100.0%; Score 562; DB 2; Length 107;
Best Local Similarity   100.0%; Pred. No. 4.1e-39;
Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

RESULT 3
AAB36225
ID   AAB36225 standard; protein; 107 AA.
XX
AC   AAB36225;
XX
DT   15-FEB-2001 (first entry)
XX
DE   Monoclonal antibody J591 kappa light chain v region #1.
XX
KW   Mouse; antibody; heavy chain; prostate cancer; biological agent.
XX
OS   Mus sp.
XX
PN   US6136311-A.
XX
PD   24-OCT-2000.
XX
PF   17-JUL-1997;   97US-00895914.
XX
PR   06-MAY-1996;   96US-0016976P.
PR   18-JUL-1996;   96US-0022125P.
PR   09-APR-1997;   97US-00838682.
XX
PA   (CORR) CORNELL RES FOUND INC.
XX
PI   Bander NH;
XX
DR   WPI; 1998-120937/11.
DR   N-PSDB; AAC66544.
XX
PT   Destroying cancer cells with agent that binds to prostate specific
PT   membrane antigen - on vascular endothelial cells near the cancer, or on
PT   normal, hypertrophic or cancerous prostatic cells, also used for
PT   diagnosis.
XX
PS   Example 12; Col 25; 35pp; English.
XX
CC   The present invention describes a method of killing cancer cells,
CC   particularly prostate cancer cells, by directing a biological agent to
CC   the cells which then binds to a prostate specific membrane antigen and
CC   causes the molecule to be internalised. The internalisation of the agent,
CC   which may be bound to a drug or which may act to kill the cell alone, and
CC   then leads to the death of the cell. The present sequence forms part of

CC   an antibody which may be used as the biological agent of the invention.
CC   In addition to prostate cancer, the method can be used with renal,
CC   urothelial, colon, renal, lung and breast cancer cells, and cancerous
CC   cells of metastatic adenocarcinoma to the liver
XX
SQ   Sequence 107 AA;

Query Match   100.0%;   Score 562;   DB 2;   Length 107;
Best Local Similarity   100.0%;   Pred. No. 4.1e-39;
Matches 107;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy  61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
       |||||||||||||||||||||||||||||||||||||||||||||||
Db  61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
```

RESULT 4
AAB10444
ID   AAB10444 standard; protein; 107 AA.
XX
AC   AAB10444;
XX
DT   01-DEC-2000 (first entry)
XX
DE   Murine monoclonal antibody MAK HE2 variable region light chain.
XX
KW   Murine; monoclonal antibody; MAK HE2; light chain; variable region;
KW   human cellular membrane antigen; tumor associated antigen; TAA; vaccine;
KW   cancer.
XX
OS   Mus sp.
XX
PN   WO200041722-A1.
XX
PD   20-JUL-2000.
XX
PF   12-JAN-2000; 2000WO-EP000174.
XX
PR   13-JAN-1999; 99CH-00000051.
XX
PA   (IGEN-) IGENEON GMBH.
XX
PI   Eckert H, Loibner H;
XX
DR   WPI; 2000-475956/41.
XX
PT   Novel use of antibodies against human cellular membrane antigens for
PT   vaccination against cancer.
XX
PS   Example 3; Page 47-48; 54pp; German.
XX
CC   This invention describes the novel use of an antibody targeted to a human
CC   cellular membrane antigen, to manufacture a medicament to
CC   prophylactically and/or therapeutically vaccinate against cancer. The
CC   antibodies against tumor associated antigen (TAA) for prophylactic and/or
CC   therapeutic vaccination against cancer may be used in low doses (when
CC   compared to antibodies against TAA for passive immunotherapy), typically
CC   less than 1 mg by injection. The antibodies also have a long continual
CC   activity that directly induces immunity and their shelf life is unlimited
CC   (fresh vaccination is always possible). This sequence represents the
CC   murine monoclonal antibody MAK HE2 variable region light chain fragment
CC   which is used in the method of the invention
XX
SQ   Sequence 107 AA;

Query Match   100.0%;   Score 562;   DB 3;   Length 107;
Best Local Similarity   100.0%;   Pred. No. 4.1e-39;
Matches 107;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy  61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
       |||||||||||||||||||||||||||||||||||||||||||||||
Db  61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
```

RESULT 5
AAR27144
ID   AAR27144 standard; protein; 109 AA.
XX
AC   AAR27144;
XX
DT   25-MAR-2003 (revised)
DT   20-MAY-1998 (first entry)
XX
DE   1E6 kappa light chain variable region.
XX
KW   Chimeric; heavy chain; variable region; monoclonal antibody;
KW   lymphocyte function associated antigen-3; LFA-3; inflammation;
KW   autoimmune disease; immunomodulation; systemic lupus erythematosus;
KW   rheumatoid arthritis; thyroiditis.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   domain   24. .34
FT   /note= "CDR1"
FT   domain   50. .56
FT   /note= "CDR2"
FT   domain   89. .97
FT   /note= "CDR3"
XX
PN   EP503646-A1.
XX
PD   16-SEP-1992.
XX
PF   12-MAR-1992; 92EP-00104318.
XX
PR   12-MAR-1991; 91US-00667975.
XX
PA   (BIOJ) BIOGEN INC.
XX
PI   Sato VL, Chisholm PL, Wallner BP;
XX
DR   WPI; 1992-309758/38.
DR   N-PSDB; AAQ28653.
XX
PT   Monoclonal antibodies active against lymphocyte function associated
PT   antigen-3 - for treating inflammation and auto:immune diseases, and for
PT   detecting LFA-3 protein in a sample.
XX
PS   Claim 19; Page 14; 30pp; English.
XX
CC   Light and heavy chain variable region sequences were deduced from the DNA
CC   sequences obtd. by PCR of DNA sequences obtd. from the hybridoma cell
CC   line 1E6-2C12 (ATCC HB 10693). The light and heavy chain regions may be
CC   used to construct a monoclonal antibody active against LFA-3 which blocks
CC   adhesion of LFA-3 expressing cells to lymphocytes. The antibody may be
CC   used in the treatment and diagnosis of acute and chronic inflammation,
CC   autoimmune diseases and for immuno- modulation including systemic lupus
CC   erythematosus, rheumatoid arthritis and thyroiditis. See also AAR27145.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 109 AA;

Query Match   100.0%;   Score 562;   DB 2;   Length 109;
Best Local Similarity   100.0%;   Pred. No. 4.2e-39;
Matches 107;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
```

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy       61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
            |||||||||||||||||||||||||||||||||||||||||||||||
Db       61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
```

RESULT 6
AAW47085
ID   AAW47085 standard; protein; 121 AA.
XX
AC   AAW47085;
XX
DT   26-JUN-1998 (first entry)
XX
DE   Mouse J591 monoclonal antibody light chain.
XX
KW   Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
KW   cancer; vascular endothelial cell; metastatic adenocarcinoma.
XX
OS   Mus sp.
XX
PN   WO9803873-A1.
XX
PD   29-JAN-1998.
XX
PF   17-JUL-1997;   97WO-US012035.
XX
PR   18-JUL-1996;   96US-0022125P.
PR   09-APR-1997;   97US-00838682.
XX
PA   (CORR) CORNELL RES FOUND INC.
XX
PI   Bander NH;
XX
DR   WPI; 1998-120937/11.
DR   N-PSDB; AAV13951.
XX
PT   Destroying cancer cells with agent that binds to prostate specific
PT   membrane antigen - on vascular endothelial cells near the cancer, or on
PT   normal, hypertrophic or cancerous prostatic cells, also used for
PT   diagnosis.
XX
PS   Example 12; Page 57; 94pp; English.
XX
CC   The present sequence represents the mouse J591 monoclonal antibody light
CC   chain from an example of the present invention. The present invention
CC   describes the elimination of cancer cells by treating vascular
CC   endothelial cells (VEC) close to the cancer with an agent (A) able to
CC   bind to the extracellular domain (ECD) of prostate specific membrane
CC   antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells.
CC   Also described are: (1) the detection of cancer tissue by detecting
CC   binding of labelled (A) to VEC close to, or within, a cancer tissue; (2)
CC   eliminating or detecting normal, benignly hyperplastic or cancerous
CC   prostate epithelial cells using optionally labelled (A); (3) hybridomas
CC   that produce a monoclonal antibody (MAb) that binds to PSMA. The method
CC   is used to treat renal, urothelial, colon, lung, rectal or breast cancers
CC   and metastatic adenocarcinoma of the liver. The diagnostic method is
CC   particularly used to detect recurrence of prostatic disease or to monitor
CC   the effect of treatments for prostate cancer (presence of PSMA in the
CC   serum indicates that prostate cells are being lysed). (A) binds to an
CC   epitope of PSMA expressed on live cells (contrast antibody 7E11 which
CC   only binds after cell lysis), allowing targeting of live, unfixed cells
CC   and thus providing more efficient treatment and diagnosis. Both cancer
CC   cells themselves and the VEC on which they depend are killed. All VEC
CC   close to cancer cells express PSMA, whatever the type of cancer, but
CC   normal VEC do not
XX
SQ   Sequence 121 AA;

Query Match   100.0%; Score 562; DB 2; Length 121;
Best Local Similarity   100.0%; Pred. No. 4.7e-39;
```

```
Qy       61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
            |||||||||||||||||||||||||||||||||||||||||||||||
Db        7 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 66

Qy       61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
            |||||||||||||||||||||||||||||||||||||||||||||||
Db       67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113
```

RESULT 7
AAY90370
ID   AAY90370 standard; protein; 121 AA.
XX
AC   AAY90370;
XX
DT   15-JAN-2001 (first entry)
XX
DE   J591 monoclonal antibody kappa light chain protein sequence #1.
XX
KW   J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
KW   prostate specific membrane antigen; prostate cancer; kappa light chain.
XX
OS   Homo sapiens.
XX
PN   US6107090-A.
XX
PD   22-AUG-2000.
XX
PF   09-APR-1997;   97US-00838682.
XX
PR   06-MAY-1996;   96US-0016976P.
PR   18-JUL-1996;   96US-0022125P.
XX
PA   (CORR) CORNELL RES FOUND INC.
XX
PI   Bander NH;
XX
DR   WPI; 1998-120937/11.
DR   N-PSDB; AAA37832.
XX
PT   Destroying cancer cells with agent that binds to prostate specific
PT   membrane antigen - on vascular endothelial cells near the cancer, or on
PT   normal, hypertrophic or cancerous prostatic cells, also used for
PT   diagnosis.
XX
PS   Example 12; Fig 10; 33pp; English.
XX
CC   This sequence is the kappa light chain of the monoclonal antibody J591.
CC   The invention relates to an isolated antibody or its antigen binding
CC   portion (I) which binds to an extracellular domain of prostate specific
CC   membrane antigen and which does not require cell lysis to bind to the
CC   extracellular domain. The antibody or its antigen binding portion is
CC   selected for its ability to bind to live cells. (I) is useful for
CC   diagnosis of diseases associated with the presence of normal, benign,
CC   hyperplastic, and cancerous epithelial cells or portions. Also it can be
CC   used for identifying the recurrence of such diseases, particularly when
CC   the disease is localised in a particular biological material of the
CC   patient for e.g. recurrence of prostatic disease. They can also be used
CC   alone or bound to a substance effective to kill cancerous prostate
CC   epithelial cells as a therapy for prostate cancer. Binding and
CC   internalising of the antibody with the prostate specific membrane
CC   antigen, permits the therapeutic use of intracellularly acting cytotoxic
CC   agents. (I) targets only prostate epithelial cells and other tissue are
CC   spared which provides safer treatment particularly for elderly patients.
CC   The antibodies bind to living prostate cells and treatments using these
CC   antibodies are more effective than those which target lysed prostate
CC   cells
XX
SQ   Sequence 121 AA;

Query Match   100.0%; Score 562; DB 2; Length 121;
```

```
Best Local Similarity  100.0%;  Pred. No. 4.7e-39;  Indels  0;  Gaps  0;
Matches 107;  Conservative  0;  Mismatches  0;

Qy    1 NIVMTQSPKSMSMSVGERVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7 NIVMTQSPKSMSMSVGERVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 66

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113

RESULT 8
AAB36222
ID   AAB36222 standard; protein; 121 AA.
XX
AC   AAB36222;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Murine monoclonal antibody J591 kappa light chain #1.
XX
KW   Mouse; antibody; heavy chain; prostate cancer; biological agent.
XX
OS   Mus sp.
XX
PN   US6136311-A.
XX
PD   24-OCT-2000.
XX
PF   17-JUL-1997;  97US-00855914.
XX
PR   06-MAY-1996;  96US-0016976P.
PR   18-JUL-1996;  96US-0022125P.
PR   09-APR-1997;  97US-0083682.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Bander NH;
XX
DR   WPI; 1998-120937/11.
DR   N-PSDB; AAC66542.
XX
PT   Destroying cancer cells with agent that binds to prostate specific
PT   membrane antigen - on vascular endothelial cells near the cancer, or on
PT   normal, hypertrophic or cancerous prostatic cells, also used for
PT   diagnosis.
XX
PS   Example 12; Fig 10; 35pp; English.
XX
CC   The present invention describes a method of killing cancer cells,
CC   particularly prostate cancer cells, by directing a biological agent to
CC   the cells which then binds to a prostate specific membrane antigen and
CC   causes the molecule to be internalised. The internalisation of the agent,
CC   which may be bound to a drug or which may act to kill the cell alone,
CC   then leads to the death of the cell. The present sequence forms part of
CC   an antibody which may be used as the biological agent of the invention.
CC   In addition to prostate cancer, the method can be used with renal,
CC   urothelial, colon, renal, lung and breast cancer cells, and cancerous
CC   cells of metastatic adenocarcinoma to the liver
XX
SQ   Sequence 121 AA;

Query Match             100.0%;  Score 562;  DB 2;  Length 121;
Best Local Similarity   100.0%;  Pred. No. 4.7e-39;
Matches 107;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 NIVMTQSPKSMSMSVGERVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7 NIVMTQSPKSMSMSVGERVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 66

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113


RESULT 9
AAW01145
ID   AAW01145 standard; protein; 127 AA.
XX
AC   AAW01145;
XX
DT   10-FEB-1997  (first entry)
XX
DE   MAb 10.1 light chain, directed against type II phospholipase A2.
XX
KW   Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis;
KW   cerebral infarction; acute kidney failure; colitis; chronic rheumatism;
KW   adult respiratory distress syndrome; cardiac shock; treatment;
KW   preclinical testing; disease; hybridoma.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    44. .54
FT                   /label= CDR 1
FT   Binding-site    70. .76
FT                   /label= CDR 2
FT   Binding-site    109. .117
FT                   /label= CDR 3
XX
PN   WO9620959-A1.
XX
PD   11-JUL-1996.
XX
PF   27-DEC-1995;  95WO-JP002714.
XX
PR   29-DEC-1994;  94JP-00340006.
XX
PA   (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
PI   Kawauchi Y, Takasaki J, Yasunaga T, Masuho Y;
XX
DR   WPI; 1996-333946/33.
DR   N-PSDB; AAT40805.
XX
PT   Monoclonal antibody inhibiting type II phospholipase A2 activity - for
PT   treatment of myocardial and cerebral infarction.
XX
PS   Claim 6; Fig 13; 69pp; Japanese.
XX
CC   Monoclonal antibodies which inhibit type II phospholipase A2 are useful
CC   in the treatment of myocardial infarction, cerebral infarction, acute
CC   kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult
CC   respiratory distress syndrome and colitis. The antibodies were generated
CC   by immunising Balb/C mice with recombinant human type II phospholipase
CC   A2. Spleen cells from the mice were fused with mouse myeloma P3U1
CC   (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase
CC   A2 inhibitory activity. Active clones were isolated including 12H5, 1.4
CC   and 10.1. These were cultured and the antibody isolated from the culture
CC   supernatant by precipitation with ammonium sulphate and purification on a
CC   column of protein A-Sepharose CL4B. Because the antibody acts on the
CC   primate and mouse forms of enzyme as well as human it is particularly
CC   suitable for preclinical testing
XX
SQ   Sequence 127 AA;

Query Match             100.0%;  Score 562;  DB 2;  Length 127;
Best Local Similarity   100.0%;  Pred. No. 4.9e-39;
Matches 107;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 NIVMTQSPKSMSMSVGERVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 NIVMTQSPKSMSMSVGERVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
         |||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        ||||||||||||||||||||||||||||||||||||||||||||||||
       81 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 127

RESULT 10
ABG74248
ID   ABG74248 standard; protein; 132 AA.
XX
AC   ABG74248;
XX
DT   22-APR-2003 (first entry)
XX
DE   Mouse antibody 3E11 light chain variable region.
XX
KW   T-cell receptor; cytostatic; dermatological; neuroprotective;
KW   immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
KW   3E11; prostate-specific membrane antigen; zeta signalling chain;
KW   CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
KW   small cell lung cancer; light chain variable region; mouse.
XX
OS   Mus sp.
XX
PN   US2002132983-A1.
XX
PD   19-SEP-2002.
XX
PF   10-DEC-2001; 2001US-00006773.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250089P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-208946/20.
DR   N-PSDB; ABX16574.
XX
PT   New chimeric molecule useful in treating patients with disorders, such as
PT   melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT   comprises GD3 and/or PSMA binding domains of antibody.
XX
PS   Disclosure; Page 18; 35pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the GD3
CC   (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC   variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC   binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC   sequences, the zeta signalling chain of the T cell receptor and an
CC   intervening CD8alpha hinge in which cysteine residues have been mutated.
CC   The chimaeric molecules expressed in T cells or NK cells or other
CC   effector cells are useful in treating patients with cancers expressing
CC   the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC   and/or together with each other or with heterologous constructs to engage
CC   additional stimulatory and functional properties of the effector cells to
CC   enhance the antitumour therapeutic efficacy (claimed). They are
CC   particularly useful in disorders including melanoma, neuroendocrine
CC   tumours and prostate and small cell lung cancer. The present sequence
CC   represents the mouse antibody 3E11 light chain variable region
XX
SQ   Sequence 132 AA;

Query Match        100.0%;    Score 562; DB 6; Length 132;
Best Local Similarity  100.0%;    Pred. No. 5.1e-39;
Matches  107; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   25 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 84

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   85 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 131
```

```
RESULT 11
ABR82783
ID   ABR82783 standard; protein; 135 AA.
XX
AC   ABR82783;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.
XX
KW   CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-196.
XX
OS   Homo sapiens.
XX
PN   WO2003072036-A2.
XX
PD   04-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005323.
XX
PR   21-FEB-2002; 2002US-0359419P.
PR   21-OCT-2002; 2002US-0420472P.
XX
PA   (UYDU-) UNIV DUKE.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Tedder T, Tuscano J;
XX
DR   WPI; 2003-712652/67.
DR   N-PSDB; ACF36433.
XX
PT   Treating a human patient diagnosed with a B-cell malignancy by
PT   administering a blocking anti-CD22 monoclonal antibody binding to the
PT   first two Ig-like domains of native human CD22 (hCD22).
XX
PS   Claim 32; Fig 23; 72pp; English.
XX
CC   The invention relates to treating a human patient diagnosed with a B-cell
CC   malignancy. The method involves (a) administering to the human patient a
CC   blocking anti-CD22 monoclonal antibody binding to the first two Ig-like
CC   domains, or to an epitope within the first two Ig-like domains of native
CC   human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the
CC   malignancy to the treatment. The method is useful for treating a human
CC   patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma,
CC   Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy
CC   cell leukemia or prolymphocytic leukemia. The present sequence represents
CC   the amino acid sequence for kappa light chain V-J junction for anti-CD22
CC   antibody from hybridoma HB22-196
XX
SQ   Sequence 135 AA;

Query Match        100.0%;    Score 562; DB 7; Length 135;
Best Local Similarity  100.0%;    Pred. No. 5.2e-39;
Matches  107; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   81 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 127

RESULT 12
ABR82893
ID   ABR82893 standard; protein; 135 AA.
XX
AC   ABR82893;
XX
DT   18-DEC-2003 (first entry)
```

```
XX
DE   Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.
XX
KW   CD22; autoimmune disease; antibody; immunosuppressive;
KW   cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer;
KW   antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic;
KW   antidiabetic; antiallergic; gene therapy; HB22-196.
XX
OS   Homo sapiens.
XX
PN   WO200072736-A2.
XX
PD   04-SEP-2003.
XX
PF   21-FEB-2003; 2003WO-US005549.
XX
PR   21-FEB-2002; 2002US-0359419P.
PR   21-OCT-2002; 2002US-0420472P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Tedder TF;
XX
DR   WPI; 2003-721765/68.
DR   N-PSDB; ACF36501.
XX
PT   Treating an autoimmune disease or a B-cell malignancy in a human patient
PT   comprises administering an amount of an anti-CD22 monoclonal antibody to
PT   the patient and monitoring the response of the disease to the treatment.
XX
PS   Claim 4; Fig 23; 69pp; English.
XX
CC   The invention relates to treating a human patient diagnosed with an
CC   autoimmune disease. The method involves administering to the patient an
CC   amount of a blocking anti-CD22 monoclonal antibody and monitoring the
CC   response of the autoimmune disease to the treatment. The method is useful
CC   in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus
CC   erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis,
CC   Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or
CC   allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The
CC   present sequence represents the amino acid sequence for kappa light chain
CC   V-J junction for anti-CD22 antibody from hybridoma HB22-196.
XX
SQ   Sequence 135 AA;

Query Match             100.0%;  Score 562;  DB 7;  Length 135;
Best Local Similarity   100.0%;  Pred. No. 5.2e-39;
Matches   107;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1  NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21  NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80

Qy         61  RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         81  RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 127

RESULT 13
ABB07176
ID   ABB07176 standard; protein; 101 AA.
XX
AC   ABB07176;
XX
DT   13-MAR-2002 (first entry)
XX
DE   Mouse 09 antibody kappa light chain 1 variable region.
XX
KW   Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4;
KW   ebvHigM MsI19D10; ebv HigM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide;
KW   antiparkinsonian; neuroprotective; nootropic; vulnerary; mouse.
XX
OS   Mus sp.
```

```
XX
PN   WO200185797-A1.
XX
PD   15-NOV-2001.
XX
PF   30-MAY-2000; 2000WO-US014902.
XX
PR   10-MAY-2000; 2000US-00568351.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI   Rodriguez M, Miller DJ, Pease LR;
XX
DR   WPI; 2002-066596/09.
DR   N-PSDB; ABA94223.
XX
PT   Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT   neurite outgrowth, regeneration, remyelination and neuroprotection in
PT   central nervous system, useful to treat post-infectious
PT   encephalomyelitis.
XX
PS   Disclosure; Fig 35A-B; 219pp; English.
XX
CC   The invention provides a neuromodulatory agent (I) capable of promoting
CC   neurite outgrowth, regeneration, remyelination and neuroprotection in
CC   central nervous system (CNS). (I) is capable of inducing remyelination,
CC   promoting cellular proliferation of glial cells, and promoting Ca2+
CC   signaling with oligodendrocytes. An humanised antibody to (I) can be
CC   selected from antibody sHIgM22 (LYM 22), ebvHigM MsI19D10, ebv HigM
CC   CB2bG8, AKJR4, CB2iE12, CB2iE7 or MSI19E5. (I) is useful for stimulating
CC   remyelination of CNS axons, stimulating proliferation of glial cells in
CC   CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC   of such therapy. (I) is capable of binding to structures and cells within
CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, or a
CC   human or domestic animal with a viral demyelinating disease, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture. (I)
CC   is also useful for stimulating remyelination of CNS axons. The antibodies
CC   are useful for preventing infection by a bacterium, virus or like
CC   pathogen that causes demyelination or other neurodegenerative condition
CC   in a subject. Methods where (I) is administered to a patient are useful
CC   for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC   disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC   disease, CNS diseases, and other conditions in the CNS where nerves are
CC   damaged as by trauma. The present sequence represents the mouse 09
CC   antibody kappa light chain 1 variable region
XX
SQ   Sequence 101 AA;

Query Match             95.0%;   Score 534;  DB 5;  Length 101;
Best Local Similarity   100.0%;  Pred. No. 8e-37;
Matches   101;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1  NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1  NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy         61  RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGG 101
               |||||||||||||||||||||||||||||||||||||||||
Db         61  RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGG 101

RESULT 14
AAW01632
ID   AAW01632 standard; protein; 136 AA.
XX
AC   AAW01632;
XX
DT   22-JUL-1997 (first entry)
XX
DE   Ber-H2 heavy kappa chain.
```

```
XX
KW   CD30; immunoglobulin; variable region; CDR; cancer; diagnosis; therapy;
KW   Ber-H2.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= sig_peptide
FT   Protein         30..136
FT                   /label= mat_protein
XX
PN   DE19543039-C1.
XX
PD   21-NOV-1996.
XX
PF   08-NOV-1995;  95DE-01043039.
XX
PR   08-NOV-1995;  95DE-01043039.
XX
PA   (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.
XX
PI   Ziegler A, Stein H;
XX
DR   WPI; 1996-507017/51.
DR   N-PSDB; AAT58329.
XX
PT   DNA mols. encoding CD30-specific immunoglobulin variable regions - useful
PT   for cancer diagnosis or therapy.
XX
PS   Claim 15; Page 15; 20pp; German.
XX
CC   The ligands are useful for diagnosis or therapy of CD30 expressing
CC   cancers, esp. Hodgkinson's disease. Cytoplasmic RNA was isolated from
CC   cells of the mouse myeloma hybrid line Ber-H2. cDNA was isolated using
CC   reverse transcriptase. A VHDJ fragment contg. band was cut from a gel and
CC   purified. DNA corresponding to VK and Vgamma was isolated and cloned into
CC   vectors. Oligonucleotides used are given in AAT58331 to AAT58340
XX
SQ   Sequence 136 AA;

Query Match             93.8%;  Score 527;  DB 2;  Length 136;
Best Local Similarity   94.4%;  Pred. No. 4.1e-36;
Matches  101; Conservative    2; Mismatches    4; Indels    0; Gaps    0;

Qy          1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
              ||||||||| |||||||||||:||||||||||||||||||||||||||||||||||||||||
Db         30 NIVMTQSPRSMSVGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89

Qy         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
              ||||||||||||||||||||||||||||| |||||| |||||||||
Db         90 RFTGSGSATDFTLTISSVQAEDLADYHCGQSYRPPTFGGGTKLEIK 136

RESULT 15
AAY71545
ID   AAY71545 standard; protein; 127 AA.
XX
AC   AAY71545;
XX
DT   12-OCT-2000  (first entry)
XX
DE   Mouse AF2 antibody light chain variable region (AF2-VL).
XX
KW   Humanised antibody; HuZAF; mouse AF2 antibody; human EU antibody; AF2-VL;
KW   light chain variable region; VL; heavy chain variable region; VH; IgG2b;
KW   gamma-interferon; IFN; complementarity determining region; CDR; FR;
KW   framework region; immunosuppressive; antiinflammatory; antisclerotic;
KW   gastrointestinal; antidiabetic; antiarthritic; dermalogical; inhibitor;
KW   autoimmune disease; graft versus host disease; organ transplant;
KW   multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis;
KW   systemic lupus erythematosus; SLE; Crohn's disease.
XX
```

```
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "N-terminal peptide"
FT   Protein         21..127
FT                   /note= "Mature mouse antibody AF2 light chain variable
FT                   region (AF2-VL)"
FT   Region          44..54
FT                   /label= CDR
FT                   /note= "Complementarity determining region"
FT   Region          70..76
FT                   /label= CDR
FT                   /note= "Complementarity determining region"
FT   Region          109..117
FT                   /label= CDR
FT                   /note= "Complementarity determining region"
XX
PN   WO200032634-A1.
XX
PD   08-JUN-2000.
XX
PF   29-NOV-1999;  99WO-US028195.
XX
PR   01-DEC-1998;  98US-0110523P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Vasquez M, Landolfi NF, Tsurushita N, Queen CL;
XX
DR   WPI; 2000-412292/35.
DR   N-PSDB; AAD01345.
XX
PT   Humanized murine AF2 immunoglobulins, useful for inhibiting gamma-
PT   interferon for the treatment of autoimmune diseases, e.g. multiple
PT   sclerosis and diabetes.
XX
PS   Claim 1; Fig 1A; 32pp; English.
XX
CC   The present amino acid sequence is the mouse AF2 antibody, light chain
CC   variable region (AF2-VL). It has IgG2b isotype and kappa light chain. It
CC   is used for the construction of humanised version of mouse AF2 antibody
CC   HuZAF, that comprises mouse antibody AF2 complementarity determining
CC   regions (CDRs), functionally joined to the human acceptor antibody EU
CC   framework region (FR). HuZAF antibody specifically binds to and
CC   neutralises gamma-interferon (IFN). They can also block the binding of
CC   mouse AF2 immunoglobulin to gamma-IFN. HuZAF does not contain sequences
CC   that are immunogenically active in humans and remains unaffected by
CC   immune responses, that may reduce its activity or circulating half-life.
CC   HuZAF may be administered to treat autoimmune diseases such as graft
CC   versus host disease following organ transplant, Type I diabetes, multiple
CC   sclerosis, rheumatoid arthritis, psoriasis, systemic lupus erythematosus
CC   (SLE), Hashimoto's thyroiditis, primary biliary cirrhosis and
CC   inflammatory bowel disease like, Crohn's disease
XX
SQ   Sequence 127 AA;

Query Match             92.7%;  Score 521;  DB 3;  Length 127;
Best Local Similarity   91.6%;  Pred. No. 1.2e-35;
Matches   98; Conservative    5; Mismatches    4; Indels    0; Gaps    0;

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Db         21 NIVMTQSPKSMYVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80

Qy         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db         81 RFTGSGSATDFTLTISSVQAEDLADYHCCGQSYNPFFTFGGSTKLEIK 127

Search completed: August 16, 2004, 11:12:18
Job time : 47.5426 secs
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        GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    August 16, 2004, 11:08:07 ; Search time 13.9148 Seconds
                                (without alignments)
                                396.996 Million cell updates/sec

Title:          US-09-889-300A-2
Perfect score:  562
Sequence:       1 NIVMTQSPKSMSMSVGERVT..........CGQGYSYPYTFGGGTKLEIK 107

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:       389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Issued_Patents_AA:*
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                4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	562	100.0	107	3	US-08-838-682-16	Sequence 16, Appl
2	562	100.0	107	3	US-08-895-914-16	Sequence 16, Appl
3	562	100.0	107	3	US-09-357-710A-16	Sequence 16, Appl
4	562	100.0	107	4	US-09-357-707-16	Sequence 16, Appl
5	562	100.0	109	5	PCT-US92-02044-2	Sequence 2, Appli
6	562	100.0	121	3	US-08-838-682-11	Sequence 11, Appl
7	562	100.0	121	3	US-08-895-914-11	Sequence 11, Appl
8	562	100.0	121	3	US-09-357-710A-11	Sequence 11, Appl
9	562	100.0	121	4	US-09-357-707-11	Sequence 11, Appl
10	521	92.7	127	4	US-09-450-520A-2	Sequence 2, Appli
11	521	92.7	136	1	US-07-634-278-99	Sequence 99, Appl
12	521	92.7	136	1	US-08-477-728-99	Sequence 99, Appl
13	521	92.7	136	1	US-08-474-040-99	Sequence 99, Appl
14	521	92.7	136	1	US-08-487-200-99	Sequence 99, Appl
15	521	92.7	136	3	US-08-484-537-99	Sequence 99, Appl
16	454	80.8	107	3	US-08-554-840-4	Sequence 4, Appli
17	454	80.8	107	4	US-08-925-339-4	Sequence 4, Appli
18	454	80.8	107	4	US-09-332-595-4	Sequence 4, Appli
19	449	79.9	107	3	US-08-554-840-2	Sequence 2, Appli
20	449	79.9	107	4	US-08-925-339-2	Sequence 2, Appli
21	449	79.9	107	4	US-09-332-595-2	Sequence 2, Appli
22	447	79.5	107	3	US-08-554-840-3	Sequence 3, Appli
23	447	79.5	107	4	US-08-925-339-3	Sequence 3, Appli
24	447	79.5	107	4	US-09-332-595-3	Sequence 3, Appli
25	444	79.0	107	3	US-08-554-840-1	Sequence 1, Appli
26	444	79.0	107	4	US-08-925-339-1	Sequence 1, Appli
27	444	79.0	107	4	US-09-332-595-1	Sequence 1, Appli
28	441	78.5	107	1	US-07-634-278-103	Sequence 103, App
29	441	78.5	107	1	US-08-477-728-103	Sequence 103, App
30	441	78.5	107	1	US-08-474-040-103	Sequence 103, App
31	441	78.5	107	1	US-08-487-200-103	Sequence 103, App
32	441	78.5	107	3	US-08-484-537-103	Sequence 103, Appli
33	441	78.5	128	4	US-09-450-520A-6	Sequence 6, Appli
34	426	75.8	108	3	US-09-157-370-4	Sequence 4, Appl
35	424.5	75.5	108	3	US-08-657-012-25	Sequence 25, Appl
36	424.5	75.5	108	3	US-09-013-872-25	Sequence 25, Appl
37	424.5	75.5	108	3	US-09-184-198-25	Sequence 25, Appl
38	424.5	75.5	108	3	US-09-633-653-25	Sequence 25, Appl
39	424	75.4	249	2	US-08-797-689-18	Sequence 18, Appl
40	424	75.4	249	4	US-09-984-186-18	Sequence 18, Appl
41	423	75.3	108	1	US-08-752-693A-1	Sequence 1, Appli
42	423	75.3	132	2	US-08-253-877C-55	Sequence 55, Appl
43	423	75.3	132	2	US-08-452-164A-55	Sequence 55, Appl
44	423	75.3	132	4	US-08-976-183A-36	Sequence 36, Appl
45	423	75.3	132	4	US-08-976-183A-37	Sequence 37, Appl

ALIGNMENTS

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RESULT 1
US-08-838-682-16
; Sequence 16, Application US/08838682
; Patent No. 6107090
; GENERAL INFORMATION:
;   APPLICANT: Bander M.D., Neil H.
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
;   TITLE OF INVENTION: CANCER
;   NUMBER OF SEQUENCES:  19
;   CORRESPONDENCE ADDRES:
;     ADDRESSE: Nixon, Hargrave, Devans & Doyle LLP
;     STREET: Clinton Square, P.C. Box 1051
;     CITY: Rochester
;     STATE: New York
;     COUNTRY: U.S.A.
;     ZIP: 14603-1051
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/838,682
;     FILING DATE:
;     CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/016,976
;     FILING DATE: 06-MAY-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/022,125
;     FILING DATE: 18-JUL-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Goldman, Michael L.
;     REGISTRATION NUMBER: 30,727
;     REFERENCE/DOCKET NUMBER: 19603/1172
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (716) 263-1304
;     TELEFAX:   (716) 263-1600
; INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 107 amino acids
;     TYPE: amino acid
;     STRANDEDNESS:
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-838-682-16

Query Match             100.0%;  Score 562;  DB 3;  Length 107;
Best Local Similarity   100.0%;  Pred. No. 3.4e-50;
Matches 107;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

RESULT 2
US-08-895-914-16
; Sequence 16, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
;   APPLICANT: Bander, Neil H.
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
;   STREET: Clinton Square, P.O. Box 1051
;   CITY: Rochester
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 14603-1051
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/895,914
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/016,976
;   FILING DATE: 06-MAY-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/022,125
;   FILING DATE: 18-JUL-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/838,682
;   FILING DATE: 09-APR-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Goldman, Michael L.
;   REGISTRATION NUMBER: 30,727
;   REFERENCE/DOCKET NUMBER: 19603/1173
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (716) 263-1304
;   TELEFAX: (716) 263-1600
;   INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-895-914-16

Query Match   100.0%;   Score 562; DB 3; Length 107;
Best Local Similarity 100.0%;   Pred. No. 3.4e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

RESULT 3

US-09-357-710A-16
; Sequence 16, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
;   APPLICANT: Bander, Neil H.
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
;   FILE REFERENCE: Lois M. Kwasigroch: BZL 242/025
;   CURRENT APPLICATION NUMBER: US/09/357,710A
;   CURRENT FILING DATE: 1999-07-20
;   PRIOR APPLICATION NUMBER: US 08/838,682
;   PRIOR FILING DATE: 1997-04-09
;   PRIOR APPLICATION NUMBER: US 60/016,976
;   PRIOR FILING DATE: 1996-05-06
;   PRIOR APPLICATION NUMBER: US 60/022,125
;   PRIOR FILING DATE: 1996-07-18
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-710A-16

Query Match   100.0%;   Score 562; DB 3; Length 107;
Best Local Similarity 100.0%;   Pred. No. 3.4e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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RESULT 4
US-09-357-707-16
; Sequence 16, Application US/09357707
; Patent No. 6649163
; GENERAL INFORMATION:
;   APPLICANT: Bander, Neil H.
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;   FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
;   CURRENT APPLICATION NUMBER: US/09/357,707
;   CURRENT FILING DATE: 1999-07-20
;   PRIOR APPLICATION NUMBER: US 08/895,914
;   PRIOR FILING DATE: 1997-07-17
;   PRIOR APPLICATION NUMBER: US 08/838,682
;   PRIOR FILING DATE: 1997-04-09
;   PRIOR APPLICATION NUMBER: US 60/016,976
;   PRIOR FILING DATE: 1996-05-06
;   PRIOR APPLICATION NUMBER: US 60/022,125
;   PRIOR FILING DATE: 1996-07-18
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-707-16

Query Match   100.0%;   Score 562; DB 4; Length 107;
Best Local Similarity 100.0%;   Pred. No. 3.4e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

RESULT 5
PCT-US92-02044-2
; Sequence 2, Application PC/TUS9202044
; GENERAL INFORMATION:
;   APPLICANT: BIOGEN, INC.
;   APPLICANT: SATO, Vicki L.
;   APPLICANT: CHISHOLM, Patricia L.
;   APPLICANT: WALLNER, Barbara P.
;   TITLE OF INVENTION: MONOCLONAL ANTIBODIES RECOGNIZING
;   TITLE OF INVENTION: LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN-3
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: c/o FISH & NEAVE
;   STREET: 875 Third Avenue
;   CITY: New York
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10022
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US92/02044
;   FILING DATE: 19920312
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/667,975
;   FILING DATE: 12-MAR-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: HALEY Jr., James F.
;   REGISTRATION NUMBER: 27,794
;   REFERENCE/DOCKET NUMBER: B150CIP
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 715-0600
;   TELEFAX: (212) 715-0673
;   TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 109 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US92-02044-2

Query Match   100.0%; Score 562; DB 5; Length 109;
Best Local Similarity   100.0%; Pred. No. 3.5e-50;
Matches 107; Conservative   0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

RESULT 6
US-08-838-682-11
; Sequence 11, Application US/08838682
; Patent No. 6107090
; GENERAL INFORMATION:
;   APPLICANT: Bander M.D., Neil H.
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
;   TITLE OF INVENTION: CANCER
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
;   STREET: Clinton Square, P.O. Box 1051

;   CITY: Rochester
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 14603-1051
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/838,682
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/016,976
;   FILING DATE: 06-MAY-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/022,125
;   FILING DATE: 18-JUL-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Goldman, Michael L.
;   REGISTRATION NUMBER: 30,727
;   REFERENCE/DOCKET NUMBER: 19603/1172
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (716) 263-1304
;   TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 121 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-838-682-11

Query Match   100.0%; Score 562; DB 3; Length 121;
Best Local Similarity   100.0%; Pred. No. 3.9e-50;
Matches 107; Conservative   0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db   67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113

RESULT 7
US-08-895-914-11
; Sequence 11, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
;   APPLICANT: Bander, Neil H.
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
;   STREET: Clinton Square, P.O. Box 1051
;   CITY: Rochester
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 14603-1051
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/895,914
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:

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;         APPLICATION NUMBER: US 60/016,976
;         FILING DATE: 06-MAY-1996
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 60/022,125
;         FILING DATE: 18-JUL-1996
;      PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 08/838,682
;         FILING DATE: 09-APR-1997
;      ATTORNEY/AGENT INFORMATION:
;         NAME: Goldman, Michael L.
;         REGISTRATION NUMBER: 30,727
;         REFERENCE/DOCKET NUMBER: 19603/1173
;      TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (716) 263-1304
;         TELEFAX:   (716) 263-1600
;   INFORMATION FOR SEQ ID NO: 11:
;      SEQUENCE CHARACTERISTICS:
;         LENGTH: 121 amino acids
;         TYPE: amino acid
;         STRANDEDNESS:
;         TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-895-914-11

Query Match             100.0%;  Score 562; DB 3; Length 121;
Best Local Similarity   100.0%;  Pred. No. 3.9e-50;
  Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy          1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Qy         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db         67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113


RESULT 8
US-09-357-710A-11
; Sequence 11, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
;   APPLICANT: Bander, Neil H.
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
;   FILE REFERENCE: Lois M. Kwasigroch: BZL 242/025
;   CURRENT APPLICATION NUMBER: US/09/357,710A
;   CURRENT FILING DATE: 1999-07-20
;   PRIOR APPLICATION NUMBER: US 08/838,682
;   PRIOR FILING DATE: 1997-04-09
;   PRIOR APPLICATION NUMBER: US 60/016,976
;   PRIOR FILING DATE: 1996-05-06
;   PRIOR APPLICATION NUMBER: US 60/022,125
;   PRIOR FILING DATE: 1996-07-18
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-710A-11

Query Match             100.0%;  Score 562; DB 3; Length 121;
Best Local Similarity   100.0%;  Pred. No. 3.9e-50;
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Db          7 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 66

Qy         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
              |||||||||||||||||||||||||||||||||||||||||||||||
Db         67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113


RESULT 9
US-09-357-707-11
; Sequence 11, Application US/09357707
; Patent No. 6649163
; GENERAL INFORMATION:
;   APPLICANT: Bander, Neil H.
;   TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;   FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
;   CURRENT APPLICATION NUMBER: US/09/357,707
;   CURRENT FILING DATE: 1999-07-20
;   PRIOR APPLICATION NUMBER: US 08/895,914
;   PRIOR FILING DATE: 1997-07-17
;   PRIOR APPLICATION NUMBER: US 08/838,682
;   PRIOR FILING DATE: 1997-04-09
;   PRIOR APPLICATION NUMBER: US 60/016,976
;   PRIOR FILING DATE: 1996-05-06
;   PRIOR APPLICATION NUMBER: US 60/022,125
;   PRIOR FILING DATE: 1996-07-18
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-707-11

Query Match             100.0%;  Score 562; DB 4; Length 121;
Best Local Similarity   100.0%;  Pred. No. 3.9e-50;
  Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db         67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113


RESULT 10
US-09-450-520A-2
; Sequence 2, Application US/0945520A
; Patent No. 6329511
; GENERAL INFORMATION:
;   APPLICANT: Vasquez, Maximiliano
;   APPLICANT: Landolfi, Nicholas F.
;   APPLICANT: Tsurushita, Naoya
;   APPLICANT: Queen, Cary L.
;   APPLICANT: Protein Design Labs, Inc.
;   TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
;   FILE REFERENCE: 011823-0081100S
;   CURRENT APPLICATION NUMBER: US/09/450,520A
;   CURRENT FILING DATE: 1999-11-29
;   PRIOR APPLICATION NUMBER: 60/110,523
;   PRIOR FILING DATE: 1998-12-01
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:
;   OTHER INFORMATION: AF2 VL
US-09-450-520A-2

Query Match              92.7%;  Score 521; DB 4; Length 127;
Best Local Similarity    91.6%;  Pred. No. 6.2e-46;
  Matches 98; Conservative   5; Mismatches   4; Indels   0; Gaps   0;

Qy          1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db   81 RFTGSGSGSATDFLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 127

RESULT 11
US-07-634-278-99
; Sequence 99, Application US/07634278
; Patent No. 5530101
  GENERAL INFORMATION:
     APPLICANT: QUEEN, Cary L.
     APPLICANT: CO, Man Sung
     APPLICANT: SCHNEIDER, William P.
     APPLICANT: LANDOLFI, Nicholas F.
     APPLICANT: COELINGH, Kathleen L.
     APPLICANT: SELICK, Harold E.
  TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
  NUMBER OF SEQUENCES: 113
  CORRESPONDENCE ADDRESS:
     ADDRESSEE: Townsend and Townsend Khourie and Crew
     STREET: 379 Lytton Avenue
     CITY: Palo Alto
     STATE: California
     COUNTRY: US
     ZIP: 94301
  COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
     SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/07/634,278
     FILING DATE: 19-DEC-1990
     CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US 07/590,274
     FILING DATE: 28-SEP-1990
  PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US 07/310,252
     FILING DATE: 13-FEB-1989
  PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US 07/290,975
     FILING DATE: 28-DEC-1988
  ATTORNEY/AGENT INFORMATION:
     NAME: Smith, William M
     REGISTRATION NUMBER: 30,223
     REFERENCE/DOCKET NUMBER: 11823-002600
  TELECOMMUNICATION INFORMATION:
     TELEPHONE: (415) 326-2400
     TELEFAX: (415) 326-2422
  INFORMATION FOR SEQ ID NO: 99:
     SEQUENCE CHARACTERISTICS:
     LENGTH: 136 amino acids
     TYPE: amino acid
     TOPOLOGY: linear
     MOLECULE TYPE: protein
US-07-634-278-99

Query Match   92.7%; Score 521; DB 1; Length 136;
Best Local Similarity   91.6%; Pred. No. 6.8e-46;
Matches   98; Conservative   5; Mismatches   4; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db   30 NIVMTQSPKSMSMVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        ||||||| |||| ||||||||||||||||||:|:||| |||| |||||
Db   90 RFTGSGSGSATDFLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 136

RESULT 12

US-08-477-728-99
; Sequence 99, Application US/08477728
; Patent No. 5585089
  GENERAL INFORMATION:
     APPLICANT: QUEEN, Cary L.
     APPLICANT: SCHNEIDER, William P.
     APPLICANT: SELICK, Harold E.
  TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
  NUMBER OF SEQUENCES: 113
  CORRESPONDENCE ADDRESS:
     ADDRESSEE: Townsend and Townsend and Crew LLP
     STREET: Two Embarcadero Center, 8th Floor
     CITY: Palo Alto
     STATE: California
     COUNTRY: US
     ZIP: 94111
  COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
     SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/08/477,728
     FILING DATE: 07-JUN-1995
     CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US 07/634,278
     FILING DATE: 19-DEC-1990
  PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US 07/590,274
     FILING DATE: 28-SEP-1990
  PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US 07/310,252
     FILING DATE: 13-FEB-1989
  PRIOR APPLICATION DATA:
     APPLICATION NUMBER: US 07/290,975
     FILING DATE: 28-DEC-1988
  ATTORNEY/AGENT INFORMATION:
     NAME: Smith, William M
     REGISTRATION NUMBER: 30,223
     REFERENCE/DOCKET NUMBER: 11823-002600
  TELECOMMUNICATION INFORMATION:
     TELEPHONE: (415) 326-2400
     TELEFAX: (415) 326-2422
  INFORMATION FOR SEQ ID NO: 99:
     SEQUENCE CHARACTERISTICS:
     LENGTH: 136 amino acids
     TYPE: amino acid
     TOPOLOGY: linear
     MOLECULE TYPE: protein
US-08-477-728-99

Query Match   92.7%; Score 521; DB 1; Length 136;
Best Local Similarity   91.6%; Pred. No. 6.8e-46;
Matches   98; Conservative   5; Mismatches   4; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
        ||||||||||||| :|:|||||| |||||| ::||||||||||||||||||||||||||||
Db   30 NIVMTQSPKSMSMVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        ||||||| |||| ||||||||||||||||||:|:||| |||| |||||
Db   90 RFTGSGSGSATDFLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 136

RESULT 13
US-08-474-040-99
; Sequence 99, Application US/08474040
; Patent No. 5693761
  GENERAL INFORMATION:
     APPLICANT: QUEEN, Cary L.
     APPLICANT: CO, Man Sung
     APPLICANT: SCHNEIDER, William P.

```
;  APPLICANT: LANDOLFI, Nicholas F.
;  APPLICANT: COELINGH, Kathleen L.
;  APPLICANT: SELICK, Harold E.
;  TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
;  NUMBER OF SEQUENCES: 113
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Townsend and Townsend Khourie and Crew
;  STREET: 379 Lytton Avenue
;  CITY: Palo Alto
;  STATE: California
;  COUNTRY: US
;  ZIP: 94301
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/474,040
;  FILING DATE: 07-JUN-1995
;  CLASSIFICATION: 536
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 07/634,278
;  FILING DATE: 19-DEC-1990
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 07/590,274
;  FILING DATE: 28-SEP-1990
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 07/310,252
;  FILING DATE: 13-FEB-1989
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 07/290,975
;  FILING DATE: 28-DEC-1988
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Smith, William M
;  REGISTRATION NUMBER: 30,223
;  REFERENCE/DOCKET NUMBER: 11823-002600
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (415) 326-2400
;  TELEFAX: (415) 326-2422
;  INFORMATION FOR SEQ ID NO: 99:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 136 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-474-040-99

Query Match         92.7%;  Score 521;  DB 1;  Length 136;
Best Local Similarity  91.6%;  Pred. No. 6.8e-46;
Matches   98;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db         30 NIVMTQSPKSMYVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89

Qy         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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RESULT 14
US-08-487-200-99
; Sequence 99, Application US/08487200
; Patent No.5693762
; GENERAL INFORMATION:
;  APPLICANT: QUEEN, Cary L.
;  APPLICANT: CO, Man Sung
;  APPLICANT: SCHNEIDER, William P.
;  APPLICANT: LANDOLFI, Nicholas F.
;  APPLICANT: COELINGH, Kathleen L.
;  APPLICANT: SELICK, Harold E.
;  TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
;  NUMBER OF SEQUENCES: 113
```

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;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Townsend and Townsend and Crew
;  STREET: 379 Lytton Avenue
;  CITY: Palo Alto
;  STATE: California
;  COUNTRY: US
;  ZIP: 94301
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/487,200
;  FILING DATE: 7-JUN-1995
;  CLASSIFICATION: 424
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 07/634,278
;  FILING DATE: 19-DEC-1990
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 07/590,274
;  FILING DATE: 28-SEP-1990
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 07/310,252
;  FILING DATE: 13-FEB-1989
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 07/290,975
;  FILING DATE: 28-DEC-1988
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Smith, William M
;  REGISTRATION NUMBER: 30,223
;  REFERENCE/DOCKET NUMBER: 11823-002610
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (415) 326-2400
;  TELEFAX: (415) 326-2422
;  INFORMATION FOR SEQ ID NO: 99:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 136 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-487-200-99

Query Match         92.7%;  Score 521;  DB 1;  Length 136;
Best Local Similarity  91.6%;  Pred. No. 6.8e-46;
Matches   98;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
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Db         90 RFTGSGSATDFTLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 136

RESULT 15
US-08-484-537-99
; Sequence 99, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
;  APPLICANT: QUEEN, Cary L.
;  APPLICANT: CO, Man Sung
;  APPLICANT: SCHNEIDER, William P.
;  APPLICANT: LANDOLFI, Nicholas F.
;  APPLICANT: COELINGH, Kathleen L.
;  APPLICANT: SELICK, Harold E.
;  TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
;  NUMBER OF SEQUENCES: 113
;  CORRESPONDENCE ADDRESS:
;  ADDRESSE: Townsend and Townsend Khourie and Crew
;  STREET: 379 Lytton Avenue
;  CITY: Palo Alto
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STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-537-99

Query Match 92.7%; Score 521; DB 3; Length 136;
Best Local Similarity 91.6%; Pred. No. 6.8e-46;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Copyright   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: August 16, 2004, 11:10:36 ; Search time 38.8655 Seconds
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Title: US-09-889-300A-2
Perfect score: 562
Sequence: 1 NIVMTQSPKSMSMSVGERVT.........CGQGYSYPYTFGGGTKLEIK 107

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
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2	562	100.0	107	10	US-09-929-546-16	Sequence 16,	Appl
3	562	100.0	121	10	US-09-929-665-11	Sequence 11,	Appl
4	562	100.0	121	10	US-09-929-546-11	Sequence 11,	Appl
5	562	100.0	128	14	US-10-010-729-70	Sequence 70,	Appl
6	562	100.0	132	13	US-10-006-773-19	Sequence 19,	Appl
7	562	100.0	135	12	US-10-372-481-31	Sequence 31,	Appl
8	562	100.0	135	15	US-10-371-797-31	Sequence 31,	Appl
9	554	98.6	128	8	US-08-779-784-34	Sequence 34,	Appl
10	534	95.0	101	14	US-10-010-729-21	Sequence 21,	Appli
11	521	92.7	127	9	US-09-992-524-2	Sequence 2,	Appli
12	512	91.1	136	12	US-10-389-417-84	Sequence 84,	Appl
13	512	91.1	136	12	US-10-452-357-99	Sequence 99,	Appl
14	512	91.1	136	15	US-10-389-155-84	Sequence 84,	Appl
15	503	89.5	107	14	US-10-160-506-48	Sequence 48,	Appl
16	503	89.5	107	16	US-10-449-379-48	Sequence 48,	Appl
17	503	89.5	107	16	US-10-688-015-48	Sequence 48,	Appl
18	490	87.2	107	14	US-10-160-506-65	Sequence 65,	Appl
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20	490	87.2	107	16	US-10-449-379-64	Sequence 64,	Appl
21	490	87.2	107	16	US-10-449-379-65	Sequence 65,	Appl
22	490	87.2	107	16	US-10-688-015-64	Sequence 64,	Appl
23	490	87.2	107	16	US-10-688-015-65	Sequence 65,	Appl
24	487	86.7	107	14	US-10-160-506-66	Sequence 66,	Appl
25	487	86.7	107	16	US-10-449-379-66	Sequence 66,	Appl
26	487	86.7	107	16	US-10-688-015-66	Sequence 66,	Appl
27	485	86.3	107	14	US-10-160-506-63	Sequence 63,	Appl
28	485	86.3	107	16	US-10-449-379-63	Sequence 63,	Appl
29	484	86.3	107	16	US-10-688-015-63	Sequence 63,	Appl
30	484	86.1	107	14	US-10-160-506-50	Sequence 50,	Appl
31	484	86.1	107	14	US-10-160-506-67	Sequence 67,	Appl
32	484	86.1	107	14	US-10-160-506-68	Sequence 68,	Appl
33	484	86.1	107	16	US-10-449-379-50	Sequence 50,	Appl
34	484	86.1	107	16	US-10-449-379-67	Sequence 67,	Appl
35	484	86.1	107	16	US-10-449-379-68	Sequence 68,	Appl
36	484	86.1	107	16	US-10-688-015-50	Sequence 50,	Appl
37	484	86.1	107	16	US-10-688-015-67	Sequence 67,	Appl
38	484	86.1	107	16	US-10-688-015-68	Sequence 68,	Appl
39	478	85.1	107	14	US-10-160-506-62	Sequence 62,	Appl
40	478	85.1	107	16	US-10-449-379-62	Sequence 62,	Appl
41	478	85.1	107	16	US-10-688-015-62	Sequence 62,	Appl
42	472	84.0	124	14	US-10-160-506-57	Sequence 57,	Appl
43	472	84.0	124	16	US-10-449-379-57	Sequence 57,	Appl
44	472	84.0	124	16	US-10-688-015-57	Sequence 57,	Appl
45	454	80.8	107	10	US-09-874-141-4	Sequence 4,	Appli

ALIGNMENTS

RESULT 1
US-09-929-665-16
; Sequence 16, Application US/09929665
; Publication No. US2003000301A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-16

Query Match   100.0%; Score 562; DB 10; Length 107;
Best Local Similarity   100.0%; Pred. No. 1.6e-48;
Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

RESULT 2
US-09-929-546-16
; Sequence 16, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-929-546-16

Query Match   100.0%; Score 562; DB 10; Length 107;
Best Local Similarity   100.0%; Pred. No. 1.6e-48;
Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

RESULT 3
US-09-929-665-11
; Sequence 11, Application US/09929665
; Publication No. US20030003101A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-929-665-11

Query Match   100.0%; Score 562; DB 10; Length 121;
Best Local Similarity   100.0%; Pred. No. 1.9e-48;
Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 66

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113

RESULT 4
US-09-929-546-11
; Sequence 11, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-929-546-11

Query Match   100.0%; Score 562; DB 10; Length 121;
Best Local Similarity   100.0%; Pred. No. 1.9e-48;
Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 66

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   67 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 113

RESULT 5
US-10-010-729-70
; Sequence 70, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 70
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-70

Query Match          100.0%;      Score 562;  DB 14;  Length 128;
Best Local Similarity 100.0%;      Pred. No. 2e-48;
Matches   107;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80

Qy    61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
           |||||||||||||||||||||||||||||||||||||||||||||
Db    81 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 127

RESULT 6
US-10-006-773-19
; Sequence 19, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-19
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;  ORGANISM: Homo sapiens
US-10-372-481-31

Query Match          100.0%;      Score 562;  DB 12;  Length 135;
Best Local Similarity 100.0%;      Pred. No. 2.1e-48;
Matches   107;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80

Qy    61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
           |||||||||||||||||||||||||||||||||||||||||||||
Db    81 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 127

RESULT 8
US-10-371-797-31
; Sequence 31, Application US/10371797
; Publication No. US2004001828A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 135
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-371-797-31
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Query Match          100.0%;      Score 562;  DB 13;  Length 132;
Best Local Similarity 100.0%;      Pred. No. 2.1e-48;
Matches   107;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    25 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 84

Qy    61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
           ||||||||||||||||||||||||||||||||||||||||||||||
Db    85 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 131

RESULT 7
US-10-372-481-31
; Sequence 31, Application US/10372481
; Publication No. US2003020297SA1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405.306
; CURRENT APPLICATION NUMBER: US/10/372,481
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 135
; TYPE: PRT
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Query Match          100.0%;      Score 562;  DB 15;  Length 135;
Best Local Similarity 100.0%;      Pred. No. 2.1e-48;
Matches   107;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80

Qy    61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
           |||||||||||||||||||||||||||||||||||||||||||||
Db    81 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 127

RESULT 9
US-08-779-784-34
; Sequence 34, Application US/08779784
; Publication No. US2002016432SA1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
```

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;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/779,784
;     FILING DATE: 07-JAN-1997
;     CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/692,084
;     FILING DATE: 08-AUG-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/236,520
;     FILING DATE: 29-APR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Jackson Esq., David A.
;     REGISTRATION NUMBER: 26,742
;     REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 201-487-5800
;     TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 128 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   FRAGMENT TYPE: N-terminal
;   ORIGINAL SOURCE:
;     ORGANISM: Mus musculus
US-08-779-784-34

Query Match       98.6%;  Score 554;  DB 8;  Length 128;
Best Local Similarity   99.1%;  Pred. No. 1.3e-47;
Matches 106;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          |||||||||||||||||||||||||||||||||||| |||||||
Db   81 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFRGTKLEIK 127
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RESULT 10
US-10-010-729-21
; Sequence 21, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
;   APPLICANT: Rodriguez, Moses
;   APPLICANT: Miller, David J.
;   APPLICANT: Pease, Larry R.
;   TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
;   TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
;   TITLE OF INVENTION: System
;   FILE REFERENCE: 1199-1-005CIP2
;   CURRENT APPLICATION NUMBER: US/10/010,729
;   CURRENT FILING DATE: 2001-11-13
;   PRIOR APPLICATION NUMBER: 09/730,473
;   PRIOR FILING DATE: 2000-12-05
;   PRIOR APPLICATION NUMBER: 09/580,787
;   PRIOR FILING DATE: 2000-05-30
;   PRIOR APPLICATION NUMBER: 09/322,862
;   PRIOR FILING DATE: 1999-05-28
;   PRIOR APPLICATION NUMBER: 08/779,784
;   PRIOR FILING DATE: 1997-01-07
;   PRIOR APPLICATION NUMBER: 08/692,084
;   PRIOR FILING DATE: 1996-08-08
;   PRIOR APPLICATION NUMBER: 08/236,520
;   PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 101
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-010-729-21

Query Match       95.0%;  Score 534;  DB 14;  Length 101;
Best Local Similarity  100.0%;  Pred. No. 9.6e-46;
Matches 101;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGG 101
          |||||||||||||||||||||||||||||||||||||||||
Db   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGG 101
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RESULT 11
US-09-992-524-2
; Sequence 2, Application US/09992524
; Patent No. US20020091240A1
; GENERAL INFORMATION:
;   APPLICANT: Vasquez, Maximiliano
;   APPLICANT: Landolfi, Nicholas F.
;   APPLICANT: Tsurushita, Naoya
;   APPLICANT: Queen, Cary L.
;   APPLICANT: Protein Design Labs, Inc.
;   TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
;   FILE REFERENCE: 011823-008110US
;   CURRENT APPLICATION NUMBER: US/09/992,524
;   CURRENT FILING DATE: 2001-11-13
;   PRIOR APPLICATION NUMBER: 09/450,520
;   PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:
;   OTHER INFORMATION: AF2 VL
US-09-992-524-2

Query Match       92.7%;  Score 521;  DB 9;  Length 127;
Best Local Similarity   91.6%;  Pred. No. 2.5e-44;
Matches 98;  Conservative 5;  Mismatches 4;  Indels 0;  Gaps 0;

Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          ||||||||||  |:|:||||| ||||||:|||||||||||||||||||||||||||||
Db   21 NIVMTQSPKSMYVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 80

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          ||||||||||||||||||||||||||||||| |:|:||| ||||||
Db   81 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYNPFTFGGSGTKLEIK 127
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RESULT 12
US-10-389-417-84
; Sequence 84, Application US/10389417
; Publication No. US20040049014A1
; GENERAL INFORMATION:
;   APPLICANT: Queen, Cary L.
;              Co, Man Sung
;              Schneider, William P.
;              Landolfi, Nicholas F.
;              Coelingh, Kathleen L.
;              Selick, Harold E.
;   TITLE OF INVENTION: Improved Humanized Immunoglobulins
```

NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Townsend and Townsend and Crew LLP
  STREET: Two Embarcadero Center, Eighth Floor
  CITY: San Francisco
  STATE: California
  COUNTRY: USA
  ZIP: 94111-3834
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/389,417
  FILING DATE: 13-Mar-2003
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/325,000
  FILING DATE: 01-JUN-1999
  APPLICATION NUMBER: US 07/290,975
  FILING DATE: 28-DEC-1988
  APPLICATION NUMBER: US 07/310,252
  FILING DATE: 13-FEB-1989
  APPLICATION NUMBER: US 07/590,274
  FILING DATE: 28-SEP-1990
  APPLICATION NUMBER: US 07/634,278
  FILING DATE: 19-DEC-1990
  APPLICATION NUMBER: US 08/484,537
  FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
  NAME: Smith, William M.
  REGISTRATION NUMBER: 30,223
  REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 84:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 136 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-389-417-84

Query Match   91.1%;   Score 512; DB 12;   Length 136;
Best Local Similarity 90.7%; Pred. No. 2.1e-43;
Matches 97; Conservative 5; Mismatches 5; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
        ||||||||||| :|:|||||| :||||||:||||||||||||||||||||||||||||| |
Db 30 NIVMTQSPKSMVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVHD 89

Qy 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        |||||||||| ||||||||||||||||||| |:|:||| |||||||
Db 90 RFTGSGSATDFLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 136

RESULT 13
US-10-452-357-99
; Sequence 99, Application US/10452357
; Publication No. US20040058414A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William
; APPLICANT: Landolfi, Nicholas
; APPLICANT: Coelingh, Kathleen
; APPLICANT: Selick, Harold
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; FILE REFERENCE: 05882.0078.CNUS01
; CURRENT APPLICATION NUMBER: US/10/452,357

; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/718,993
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 09/487,200
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/634,278
; PRIOR FILING DATE: 1990-12-19
; PRIOR APPLICATION NUMBER: 07/590,275
; PRIOR FILING DATE: 1990-09-28
; PRIOR APPLICATION NUMBER: 07/310,252
; PRIOR FILING DATE: 1989-02-13
; PRIOR APPLICATION NUMBER: 07/290,975
; PRIOR FILING DATE: 1988-12-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: AF2 light chain antibody
US-10-452-357-99

Query Match   91.1%;   Score 512; DB 12;   Length 136;
Best Local Similarity 90.7%; Pred. No. 2.1e-43;
Matches 97; Conservative 5; Mismatches 5; Indels   0; Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
        ||||||||||| :|:|||||| :||||||:||||||||||||||||||||||||||||| |
Db 30 NIVMTQSPKSMVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVHD 89

Qy 61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        |||||||||| ||||||||||||||||||| |:|:||| |||||||
Db 90 RFTGSGSATDFLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 136

RESULT 14
US-10-389-155-84
; Sequence 84, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
;   Co, Man Sung
;   Schneider, William P.
;   Landolfi, Nicholas F.
;   Coelingh, Kathleen L.
;   Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulin
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/389,155
;   FILING DATE: 13-Mar-2003
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/325,000
;   FILING DATE: 01-JUN-1999
;   APPLICATION NUMBER: US 07/290,975
;   FILING DATE: 28-DEC-1988
;   APPLICATION NUMBER: US 07/310,252
;   FILING DATE: 13-FEB-1989
;   APPLICATION NUMBER: US 07/590,274
;   FILING DATE: 28-SEP-1990

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;        APPLICATION NUMBER: US 07/634,278
;        FILING DATE: 19-DEC-1990
;        APPLICATION NUMBER: US 08/484,537
;        FILING DATE: 07-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Smith, William M.
;        REGISTRATION NUMBER: 30,223
;        REFERENCE/DOCKET NUMBER: 011823-002650US
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: (415) 576-0200
;        TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 84:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 136 amino acids
;        TYPE: amino acid
;        TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-389-155-84

Query Match         91.1%;   Score 512; DB 15; Length 136;
Best Local Similarity   90.7%;   Pred. No. 2.1e-43;
Matches  97;  Conservative   5;  Mismatches   5;  Indels   0;  Gaps   0;

Qy      1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db     30 NIVMTQSPKSMVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVHD 89

Qy     61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
            ||||||||||||||||||||||||||| |:|:|||||||||||||
Db     90 RFTGSGSATDFLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK 136


RESULT 15
US-10-160-506-48
; Sequence 48, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
;     APPLICANT: Bander, Neil H.
;     TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
;     TITLE OF INVENTION:  SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
;     TITLE OF INVENTION:  PROSTATE SPECIFIC MEMBRANE ANTIGEN
;     FILE REFERENCE: 10448-162001
;     CURRENT APPLICATION NUMBER: US/10/160,506
;     CURRENT FILING DATE: 2002-05-30
;     PRIOR APPLICATION NUMBER: 60/324,100
;     PRIOR FILING DATE: 2001-09-20
;     PRIOR APPLICATION NUMBER: 60/362,612
;     PRIOR FILING DATE: 2002-03-08
;     NUMBER OF SEQ ID NOS: 128
;     SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 48
;     LENGTH: 107
;     TYPE: PRT
;     ORGANISM: Mus musculus
US-10-160-506-48

Query Match         89.5%;   Score 503; DB 14; Length 107;
Best Local Similarity   87.9%;   Pred. No. 1.3e-42;
Matches  94;  Conservative   7;  Mismatches   6;  Indels   0;  Gaps   0;

Qy      1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
            ||||||||||| |||||||||||||||||||||| |:|||||||||||||||||||||
Db      1 NIVMTQFPKSMSISVGERVTLTCKASENVGTYVSWYQQKPEQSPKMLIYGASNRFTGVPD 60

Qy     61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
            ||||||||||||||||||| :::|| ||||| |:||||||||| |
Db     61 RFTGSGSATDFILTISSVQTEDLVDYCGQSYFPYTFPYTFGGGTKLEMK 107
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Search completed: August 16, 2004, 11:21:20
Job time : 39.8655 secs

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:  August 16, 2004, 11:08:06 ; Search time 11.5157 Seconds
                                  (without alignments)
                                  893.780 Million cell updates/sec

Title:          US-09-889-300A-2
Perfect score:  562
Sequence:       1 NIVMTQSPKSMSMSVGERVT........CGQGYSYPYTFGGGTKLEIK 107
Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:  283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:   283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR 78:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	562	100.0	136	1	KVMS21	Ig kappa chain pre
2	551	98.0	111	2	D37266	Ig kappa chain V r
3	515	91.6	107	2	S33132	Ig kappa chain V r
4	498	88.6	118	2	I33932	Ig kappa chain pre
5	494	87.9	107	2	S38713	Ig light chain V r
6	459	81.7	107	2	PL0268	Ig kappa chain V r
7	454	80.8	96	2	PH1070	Ig light chain V r
8	446.5	79.4	91	2	PH1071	Ig light chain V r
9	440	78.3	108	2	PL0204	anti-DNA autoantib
10	432	76.9	107	2	S32192	Ig kappa chain V r
11	432	76.3	117	2	S42466	Ig kappa chain V r
12	427	76.0	107	2	S32191	Ig kappa chain V r
13	422	75.1	149	1	KVMS11	Ig kappa chain pre
14	419	74.6	127	2	S04577	Ig kappa chain pre
15	416	74.0	119	2	PQ0265	Ig kappa chain V r
16	410	73.0	107	2	A28195	Ig kappa chain V r
17	410	73.0	214	2	S62212	Ig kappa chain (Ma
18	409	72.8	152	2	S30751	Ig kappa chain pre
19	407	72.4	113	2	H30534	Ig kappa chain pre
20	407	72.4	131	2	PL0207	anti-idiotypic ant
21	404	71.9	113	2	F30534	Ig kappa chain V r
22	403	71.7	114	1	KVMS7A	Ig kappa chain V r
23	403	71.7	135	2	S38807	Ig light chain V-J
24	401	71.4	113	2	PL0264	Ig kappa chain V r
25	399.5	70.5	225	2	S37484	Ig kappa chain - m
26	396	70.5	128	2	A47159	Ig lambda chain V
27	395	70.3	107	2	D53285	Ig kappa chain V a
28	395	70.3	112	2	E30538	Ig kappa chain V r
29	395	70.3	112	2	F30538	Ig kappa chain V r
30	394	70.1	107	2	B28195	Ig kappa chain V r
31	394	70.1	113	2	JC2270	PL7-6 antibody lig
32	393	69.9	109	2	S26336	Ig light chain V r
33	392	69.8	100	2	H38601	Ig kappa chain V r
34	392	69.8	113	2	PL0263	Ig kappa chain V r
35	391	69.6	134	2	PC1214	Ig kappa chain pre
36	389.5	69.3	108	2	PL0083	Ig kappa chain V r
37	389	69.2	129	2	S52793	Ig kappa chain V r
38	388.5	69.1	118	2	PT0356	Ig kappa chain V r
39	387	68.9	108	2	B49047	Ig kappa chain V r
40	385	68.5	129	2	S40317	Ig kappa chain - h
41	384	68.3	109	2	S31981	Ig kappa chain - h
42	384	68.3	114	1	K4HULN	Ig kappa chain V-I
43	383	68.1	111	2	B37266	Ig kappa chain V r
44	382.5	68.1	112	2	S41393	Ig kappa chain V r
45	382.5	68.1	113	2	PT0407	Ig light chain V r

ALIGNMENTS

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RESULT 1
KVMS21
Ig kappa chain precursor V region (MOPC 21) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
A;Accession: A93736; A90262; B49982; A01917
R;Hamlyn, P.H.; Gait, M.J.; Milstein, C.
Nucleic Acids Res. 9, 4485-4494, 1981
A;Title: Complete sequence of an immunoglobulin mRNA using specific priming and the did
A;Reference number: A93736; MUID:82059477; PMID:6170937
A;Accession: A93736
A;Molecule type: mRNA
A;Residues: 1-136 <HAM>
R;Svasti, J.; Milstein, C.
Biochem. J. 128, 427-444, 1972
A;Title: The complete amino acid sequence of a mouse kappa light chain.
A;Reference number: A90262; MUID:73053310; PMID:4638343
A;Contents: myeloma protein MOPC 21
A;Accession: A90262
A;Molecule type: protein
A;Residues: 30-136 <SVA>
R;Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R
J. Biol. Chem. 269, 2805-2813, 1994
A;Title: Topology of an amiloride-binding protein.
A;Reference number: A49982; MUID:9413Z051; PMID:8300613
A;Accession: B49982
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 30-136 <LIN>
A;Cross-references: GB:L24803; NID:g452098; PIDN:AAC37684.1; PID:g452099
A;Experimental source: clone BA7.1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-136/Product: Ig kappa chain V region (MOPC 21) #status experimental <IMM>
F;45-119/Domain: immunoglobulin homology <IMM>
F;125-136/Region: J segment (JK2)
F;52-117/Disulfide bonds: #status predicted

Query Match               100.0%;   Score 562;   DB 1;   Length 136;
Best Local Similarity   100.0%;   Pred. No. 1.3e-42;
Matches 107;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db  30 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89

Qy  61 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  90 RFTGSGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 136
```

A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated ger[
A;Reference number: A33932; MUID:89282823; PMID:2499887
A;Accession: I33932
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-118 <BAC>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;39-113/Domain: immunoglobulin homology <IMM>

Query Match   88.6%; Score 498; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 4.8e-37;
Matches   95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   24 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 83

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYP 95
        |||||||||||||||||||||||||||||||||||
Db   84 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYP 118
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RESULT 5
S38713
Ig light chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38713
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <CIM>
A;Cross-references: EMBL:X76019; NID:g416090; PIDN:CAA53606.1; PID:g1333952
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   87.9%; Score 494; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 9.8e-37;
Matches   95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db    1 DIVLTQSPKSMSMSVGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRNTGVPE 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        ||||||||||||||||||||||||||||:||:
Db   61 RFTGSGSATDFTLTISSVQAEDLADYYCCQGSYIPLTFGAGTKLEIK 107
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RESULT 6
PL0268
Ig kappa chain V region (anti-DNA, DP9VK and DP17VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0268
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat[
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0268
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2

RESULT 2
D37266
Ig kappa chain V region (129) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: D37266
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti[
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: D37266
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

Query Match   98.0%; Score 551; DB 2; Length 111;
Best Local Similarity 98.1%; Pred. No. 9.9e-42;
Matches   105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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        :|||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4 DIVMTQIPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 63

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||||||||||||||||||||||
Db   64 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 110
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RESULT 3
S33132
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S33132
R;Tempst, P.R.; Barbanti, E.; Bremner, P.; Carr, F.J.; Ghislieri, M.; Rifaldi, B.; Marc[
submitted to the EMBL Data Library May 1993
A;Description: A humanized anti-tumor necrosis factor alpha monoclonal antibody that act[
A;Reference number: S33131
A;Accession: S33132
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <TEM>
A;Cross-references: EMBL:Z22670; NID:g297473; PIDN:CAA80379.1; PID:g297474
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   91.6%; Score 515; DB 2; Length 107;
Best Local Similarity 92.5%; Pred. No. 1.4e-38;
Matches   99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db    1 NIVMTQSPKSMSMSVGERVTLSCKASENVDTFVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        ||||||||||||||||||||||||||||||:||:
Db   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQSYIFPPTLGGGTKLEIK 107
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RESULT 4
I33932
Ig kappa chain precursor V region (E7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: I33932
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match   81.7%;   Score 459;   DB 2;   Length 107;
Best Local Similarity 82.2%;   Pred. No. 1.2e-33;
Matches 88;   Conservative 7;   Mismatches 12;   Indels 0;   Gaps 0;

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Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
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Db   1 NIVMAWSPKSMSMSVGERVTLSCKASENVGTYVSWYQQTPEQSPTLLIYRASDRYFGVPD 60

Qy  61 RFTGGGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
       || ||||| || ||||||| |||||| ||:|| :| ||||||||| |
Db  61 RFAGGGSAADFSLTISSVHAEDLADYYCEQGSYNYPWTFGGGTKLEVK 107
```

RESULT 7
PH1070
Ig light chain V region (clone 17s.5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1070
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1070
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-96 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   80.8%;   Score 454;   DB 2;   Length 96;
Best Local Similarity 93.9%;   Pred. No. 2.9e-33;
Matches 92;   Conservative 1;   Mismatches 3;   Indels 2;   Gaps 2;

```
Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
       ||||||||||||||||||||| ||||||| ||||||||| ||||||||||||||||||||
Db   1 NIVMTQSPKSMSMSVGERVTLSCKASENVGTYVSWYQQKSEQSPKLLIYGASNRYTGVPD 60

Qy  61 RFTGGGSATDFLTISSVQAEDLADYHCGQGYSYPYTF 98
       |||||||||||||||||||||||||||||  || ||
Db  61 RFTGGGSATDFLTISSVQAEDLADYHCGQ-YS-PRTF 96
```

RESULT 8
PH1071
Ig light chain V region (clone 165.3m) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1071
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1071
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-91 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: immunoglobulin
F;10-83/Domain: immunoglobulin homology <IMM>

Query Match   79.4%;   Score 446.5;   DB 2;   Length 91;
Best Local Similarity 93.5%;   Pred. No. 1.3e-32;
Matches 86;   Conservative 3;   Mismatches 3;   Indels 2;   Gaps 1;

```
Qy   7 SPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSG 66
       |||||||||||||| ||||||| ||||||||| |  |||:|||||||||||||||||||||
Db   1 SPKSMSMSVGERVTLSCKASENVGTYVSWYQQKP-QSPQLLIYGASNRYTGVPDRFTGSG 59

Qy  67 SATDFLTISSVQAEDLADYHCGQGYSYPYTF 98
       |||||||||||||||||||||||||||||:||
Db  60 SATDFLTISSVQAEDLADYHCGQGYSYPPTF 91
```

RESULT 9
PL0204
anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0204
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from
A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0204
A;Molecule type: mRNA
A;Residues: 1-108 <SMI>
A;Cross-references: GB:X53644; NID:g50198; PIDN:CAA37695.1; PID:g930144
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;50-56/Region: complementarity-determining 2
F;89-97/Region: complementarity-determining 3
F;96-108/Region: JH region

Query Match   78.3%;   Score 440;   DB 2;   Length 108;
Best Local Similarity 79.4%;   Pred. No. 5.5e-32;
Matches 85;   Conservative 9;   Mismatches 13;   Indels 0;   Gaps 0;

```
Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
       :||||||:: :|:|:|||:|:| ||||:||| |:||||||||| ||| ||: |||||||||
Db   1 DIVMTQSQKFMSTSVGDRVSVTCKASQNVNTYVAWYQQKPGQSPKALIYSASRYTGVPD 60

Qy  61 RFTGGGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
       |||||||:||| | :||||| |||:| ||| || ||||||||||||
Db  61 RFTGGGSGTDFTLAISSVQSEDLAEYFCQQYNSYPYTFGGGTKLEIK 107
```

RESULT 10
S32192
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32192
R;Izui, S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <IZU>
A;Cross-references: EMBL:X70097; NID:g288262; PIDN:CAA49701.1; PID:g288263
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   76.9%;   Score 432;   DB 2;   Length 107;
Best Local Similarity 79.4%;   Pred. No. 2.8e-31;
Matches 85;   Conservative 8;   Mismatches 14;   Indels 0;   Gaps 0;

```
Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
       :||||||: :|:|:|||:|:| ||||:|| :  ||||||||| |||||||:||:|||||||
Db   1 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYRYTGVPD 60

Qy  61 RFTGGGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
       |||||||:||| |::||||||||:| |||| ||| ||||||||||||
Db  61 RFTGGGSGTDFTFTISSVQAEDLAVYYCQQHYSTPYTFGGGTKLEIK 107
```

RESULT 11
S42466
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
A;Accession: S42466
R;Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A;Reference number: S42466
A;Accession: S42466
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <SHI>
A;Cross-references: EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID:g460825
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match   76.3%;   Score 429;   DB 2;   Length 117;
Best Local Similarity   78.5%;   Pred. No. 5.5e-31;
Matches   84;   Conservative   10;   Mismatches   13;   Indels   0;   Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          :||||| ||||||||||||||||||:|||:: ::|||||| ||||||| | |:|:||||||
Db   11 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 70

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          ||||||| ||||||||||| ||||| || :||:| ||||||||||||
Db   71 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 117

RESULT 12
S32191
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
A;Accession: S32191
R;Izui. S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Accession: S32191
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <IZU>
A;Cross-references: EMBL:X70095; NID:g288260; PIDN:CAA49700.1; PID:g288261
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   76.0%;   Score 427;   DB 2;   Length 107;
Best Local Similarity   78.5%;   Pred. No. 7.6e-31;
Matches   84;   Conservative   8;   Mismatches   15;   Indels   0;   Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          :||||| ||||||||||||||||||:|||:: ::|||||| ||||||| | |:|:||||||
Db   1 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYWASYRYTGVPD 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
Db   61 RFTGSGSGTDFTFTISSVQPEDLAVYYCQQHYSTPYTFGGGTKLEIK 107

RESULT 13
KVMS11
Ig kappa chain precursor V region (MPC11) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 21-Jan-2000
A;Accession: A90823; A90753; A90298; A01916
R;Kelley, D.E.; Coleclough, C.; Perry, R.P.
Cell 29, 681-689, 1982
A;Title: Functional significance and evolutionary development of the 5'-terminal regions
A;Reference number: A90823; MUID:83001944; PMID:6288267

A;Accession: A90823
A;Molecule type: DNA
A;Residues: 1-71 <KEL>
A;Note: the sequence was determined from the differentiated gene
R;Rabbitts, T.H.; Hamlyn, P.H.; Matthyssens, G.; Roe, B.A.
Can. J. Biochem. 58, 176-187, 1980
A;Title: The variability, arrangement, and rearrangement of immunoglobulin genes.
A;Reference number: A90753; MUID:80176554; PMID:6245773
A;Accession: A90753
A;Molecule type: mRNA
A;Residues: 41-149 <RAB>
R;Smith, G.P.
Biochem. J. 171, 337-347, 1978
A;Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC
A;Reference number: A90298; MUID:78186617; PMID:418775
A;Contents: myeloma protein MPC11
A;Accession: A90298
A;Molecule type: protein
A;Residues: 30-149 <SMI>
A;Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not
C;Comment: The mature chain has 12 additional residues at its amino end, due to a tan
42 corresponds to the amino-terminal residue of typical kappa chains.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: duplication; heterotetramer; immunoglobulin
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>
F;57-131/Domain: immunoglobulin homology <IMM>
F;64-129/Disulfide bonds: #status predicted

Query Match   75.1%;   Score 422;   DB 1;   Length 149;
Best Local Similarity   78.5%;   Pred. No. 2.9e-30;
Matches   84;   Conservative   8;   Mismatches   15;   Indels   0;   Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          :||||| ||||||||||||||||||:|||:: ::|||||| |||||||:|| |:||||||
Db   42 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPD 101

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          ||||||| ||||||||||||||||| || :||:| ||||||||||||
Db 102 RFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIK 148

RESULT 14
S04577
Ig kappa chain precursor V region (MRL-RF28L) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S04577
R;Kofler, R.; Duchosal, M.A.; Dixon, F.J.
submitted to the EMBL Data Library, March 1989
A;Description: Complexity, polymorphism and connectivity of murine V(kappa) gene fami
A;Reference number: S04577
A;Accession: S04577
A;Molecule type: mRNA
A;Residues: 1-127 <KOF>
A;Cross-references: EMBL:X14622; NID:g52400; PIDN:CAA32775.1; PID:g52401
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence predicted <SIG>
F;21-127/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match   74.6%;   Score 419;   DB 2;   Length 127;
Best Local Similarity   75.7%;   Pred. No. 4.5e-30;
Matches   81;   Conservative   10;   Mismatches   16;   Indels   0;   Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          |||||: ||:| :::|:|||:|||||||:: :: ||||||| |||||||:||||||||||
Db   21 SIVMTQTPKFLPVSAGDRVTMTCKASQSVGNNVAWYQQKPGQSPKLLIYYASNRYTGVPD 80

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107

```
Db         81 RFTGSGSGTDFTFTISSVQVEDLAVYFCQQHYSSPWTFGGGTKLEIK 127
              ||||||| |||| ||||| ||||| |||||  | || | ||||||||||
```

RESULT 15
PQ0265
Ig kappa chain V region (MC1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PQ0265
R;Lohman, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 105, 283-284, 1991
A;Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal
A;Reference number: PQ0265; MUID:92039046; PMID:1937027
A;Accession: PQ0265
A;Molecule type: mRNA
A;Residues: 1-119 <LOH>
A;Cross-references: GB:M59985
C;Comment: This protein recognizes a restricted idiotype associated with antibodies spec
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;28-102/Domain: immunoglobulin homology <IMM>
F;36-46/Region: complementarity-determining 1
F;62-68/Region: complementarity-determining 2
F;101-109/Region: complementarity-determining 3

Query Match   74.0%;   Score 416;   DB 2;   Length 119;
Best Local Similarity   77.6%;   Pred. No. 7.8e-30;
Matches   83;   Conservative   8;   Mismatches   16;   Indels   0;   Gaps   0;

Qy   1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
           :||||| :|||: |:|||| : :||||| |:|||| |||||| || |||| ||||||
Db   13 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPD 72

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
           |||||| || ||||||||| || | || | | | |||||||||||
Db   73 RFTGSGSGTDLTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIK 119

Search completed: August 16, 2004, 11:09:11
Job time : 11.5157 secs
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OM protein - protein search, using sw model

Run on:   August 16, 2004, 11:08:06 ; Search time 7.67713 Seconds
                                       (without alignments)
                                       725.728 Million cell updates/sec

Title:          US-09-889-300A-2
Perfect score:  562
Sequence:       1 NIVMTQSPKSMSMSVGERVT.........CGQGYSYPYTFGGGTKLEIK 107

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:        141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	562	100.0	136	1	KV5B_MOUSE	P01634	mus musculu
2	422	75.1	149	1	KV5A_MOUSE	P01633	mus musculu
3	403	71.7	114	1	KV1A_MOUSE	P01632	mus musculu
4	383	68.1	114	1	KV4A_HUMAN	P01625	homo sapien
5	376	66.9	134	1	KV4C_HUMAN	P06314	homo sapien
6	375	66.7	108	1	KV1M_HUMAN	P01605	homo sapien
7	370	65.8	108	1	KV1Y_HUMAN	P80362	homo sapien
8	365	64.9	108	1	KV1O_HUMAN	P04430	homo sapien
9	363	64.6	108	1	KV1V_HUMAN	P06313	homo sapien
10	362.5	64.5	133	1	KV4B_HUMAN	P01600	homo sapien
11	359	63.9	108	1	KV1H_HUMAN	P01662	mus musculu
12	359	63.9	111	1	KV3J_MOUSE	P04432	homo sapien
13	359	63.9	129	1	KV1X_HUMAN	P01604	homo sapien
14	358	63.7	108	1	KV1L_HUMAN	P01660	mus musculu
15	358	63.7	111	1	KV3H_MOUSE	P04431	homo sapien
16	358	63.7	129	1	KV1W_HUMAN	P01606	homo sapien
17	357	63.5	108	1	KV1N_HUMAN	P18136	homo sapien
18	356.5	63.4	129	1	KV1M_HUMAN	P18135	homo sapien
19	355.5	63.3	129	1	KV3L_HUMAN	P01661	mus musculu
20	354	63.0	131	1	KV3I_MOUSE	P01597	homo sapien
21	353	62.8	108	1	KV1E_HUMAN	P01664	mus musculu
22	353	62.8	111	1	KV3L_MOUSE	P01620	homo sapien
23	352.5	62.7	109	1	KV3B_HUMAN	P01624	homo sapien
24	352.5	62.7	109	1	KV3F_HUMAN	P01593	homo sapien
25	350	62.3	108	1	KV1A_HUMAN	P01623	homo sapien
26	349.5	62.2	109	1	KV3E_HUMAN	P01603	homo sapien
27	349	62.1	108	1	KV1K_HUMAN	P01608	homo sapien
28	349	62.1	108	1	KV1P_HUMAN	P01594	homo sapien
29	348	61.9	108	1	KV1B_HUMAN	P01611	homo sapien
30	348	61.9	108	1	KV1S_HUMAN	P01646	mus musculu
31	348	61.9	108	1	KV5M_MOUSE	P01610	homo sapien
32	347	61.7	108	1	KV1R_HUMAN	P04207	homo sapien
33	344.5	61.3	129	1	KV3H_HUMAN	P01622	homo sapien
34	343.5	61.1	109	1	KV3D_HUMAN	P01663	mus musculu
35	343	61.0	111	1	KV3K_MOUSE	P01631	mus musculu
36	342.5	60.9	113	1	KV2G_MOUSE	P01599	homo sapien
37	342	60.9	108	1	KV1Q_HUMAN	P01609	homo sapien
38	342	60.9	108	1	KV5U_MOUSE	P04946	mus musculu
39	342	60.9	111	1	KV3M_MOUSE	P01665	mus musculu
40	342	60.9	108	1	KV1C_HUMAN	P01595	homo sapien
41	341	60.7	108	1	KV5K_MOUSE	P01644	mus musculu
42	341	60.7	108	1	KV3A_HUMAN	P01619	homo sapien
43	339.5	60.4	108	1	KV3D_MOUSE	P03977	mus musculu
44	339	60.3	111	1	KV3D_MOUSE	P01667	mus musculu
45	339	60.3	111	1	KV3O_MOUSE		

ALIGNMENTS

```
RESULT 1
KV5B_MOUSE
ID   KV5B_MOUSE     STANDARD;      PRT;    136 AA.
AC   P01634;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig kappa chain V-v region MOPC 21 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82059477; PubMed=6170937;
RA   Hamlyn P.H. Gait M.J., Milstein C.;
RT   "Complete sequence of an immunoglobulin mRNA using specific priming
RT   and the dideoxynucleotide method of RNA sequencing.";
RL   Nucleic Acids Res. 9:4485-4494(1981).
RN   [2]
RP   SEQUENCE OF 30-136.
RX   MEDLINE=73053310; PubMed=4638343;
RA   Svasti J., Milstein C.;
RT   "The complete amino acid sequence of a mouse kappa light chain.";
RL   Biochem. J. 128:427-444(1972).
CC   -------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   -------------------------------------------------------------------------
DR   EMBL; V00810; CAA24192.1; ALT_TERM.
DR   PIR; A93736; KVMS21.
DR   PDB; 1IGC; 03-JUN-95.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; 3D-structure.
FT   SIGNAL         1     29
FT   CHAIN         30    136       IG KAPPA CHAIN V-V REGION MOPC 21.
FT   DOMAIN        30     52       FRAMEWORK-1.
FT   DOMAIN        53     63       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        64     78       FRAMEWORK-2.
FT   DOMAIN        79     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        86    117       FRAMEWORK-3.
FT   DOMAIN       118    126       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       127    136       FRAMEWORK-4.
FT   NON_TER      136    136
SQ   SEQUENCE     136 AA;   14902 MW;  8CDD85113996D1C2 CRC64;

Query Match             100.0%;  Score 562;  DB 1;  Length 136;
```

```
Best Local Similarity  100.0%;  Pred. No. 7e-53;
Matches 107;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   30 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 89

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||||||||||||||||||||||
Db   90 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 136

RESULT 2
ID   KV5A_MOUSE      STANDARD;      PRT;      149 AA.
AC   P01633;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-v region MPC11 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 1-71 FROM N.A.
RX   MEDLINE=83001944; PubMed=6288267;
RA   Kelley D.E., Coleclough C., Perry R.P.;
RT   "Functional significance and evolutionary development of the
RT   5'-terminal regions of immunoglobulin variable-region genes.";
RL   Cell 29:681-689(1982).
RN   [2]
RP   SEQUENCE OF 41-149 FROM N.A.
RX   MEDLINE=80176554; PubMed=6245773;
RA   Rabbits T.H., Hamlyn P.H., Matthyssens G., Roe B.A.;
RT   "The variability, arrangement, and rearrangement of immunoglobulin
RT   genes.";
RL   Can. J. Biochem. 58:176-187(1980).
RN   [3]
RP   SEQUENCE OF 30-149.
RX   MEDLINE=78186617; PubMed=418775;
RA   Smith G.P.;
RT   "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT   myeloma MPC 11.";
RL   Biochem. J. 171:337-347(1978).
-!- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC       AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC       CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC       RESIDUE OF TYPICAL KAPPA CHAINS.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; J00561; AAA38776.1; -.
DR   PIR; A90823; KVMS11.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal; Repeat.
FT   SIGNAL        1     29
FT   CHAIN        30    149       IG KAPPA CHAIN V-v REGION MPC11.
FT   DOMAIN       42     64       FRAMEWORK-1.
FT   DOMAIN       65     75       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       76     90       FRAMEWORK-2.
FT   DOMAIN       91     97       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       98    129       FRAMEWORK-3.
FT   DOMAIN      130    138       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      139    148       FRAMEWORK-4.
FT   REPEAT       26     35
FT   REPEAT       38     47
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;   16434 MW;   B04B0C87B682AC3E CRC64;

Query Match             75.1%;  Score 422;  DB 1;  Length 149;
Best Local Similarity   78.5%;  Pred. No. 6.2e-38;
Matches  84;  Conservative   8;  Mismatches  15;  Indels   0;  Gaps   0;

Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
        :|||||||||||||||||| :| |:||||||||||:||::|||||:||||||YSASYRYTGVPD
Db   42 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPD 101

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        |||||| ||||||||| ||||||||||::|||||| ||||||||||||
Db  102 RFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIK 148

RESULT 3
ID   KV1A_MOUSE      STANDARD;      PRT;      114 AA.
AC   P01632;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region S107A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81241357; PubMed=6788890;
RA   Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT   "Nucleic acid and protein sequences of phosphocholine-binding light
RT   chains.";
RL   J. Exp. Med. 153:1366-1370(1981).
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U29423; AAC00033.1; -.
DR   PIR; A01915; KVMS7A.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     40       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       41     55       FRAMEWORK-2.
FT   DOMAIN       56     62       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       63     94       FRAMEWORK-3.
FT   DOMAIN       95    103       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      104    113       FRAMEWORK-4.
FT   DISULFID     23     94       BY SIMILARITY.
FT   NON_TER     114    114
SQ   SEQUENCE   114 AA;   12717 MW;   3200EBC8E9DBE67B CRC64;

Query Match             71.7%;  Score 403;  DB 1;  Length 114;
Best Local Similarity   67.3%;  Pred. No. 4.8e-36;
Matches  76;  Conservative  16;  Mismatches  15;  Indels   6;  Gaps   1;
```

```
Qy    1 NIVMTQSPKSMSVGERVTLTCKASENV------VTVSWYQQKPEQSPKLLIYGASNR 54
        :|||||||  :::  ::||:|: :||:||::|||||||||||
Db    1 DIVMTQSPTFLAVTASKKVTISCTASESLYSSKHKVHYLAWYQKKPEQSPKLLIYGASNR 60

Qy   55 YTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        |||||||||||||||||||||||| |:|| ||| ||||
Db   61 YIGVPDRFTGSGSGTDFTLTISSVQVEDLTHYYCAQFYSYPLTFGAGTKLEIK 113
```

RESULT 4
KV4A_HUMAN
ID   KV4A_HUMAN   STANDARD;   PRT;   114 AA.
AC   P01625;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig kappa chain V-IV region Len.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76004342; PubMed=50995;
RA   Schneider M., Hilschmann N.;
RT   "The primary structure of a monoclonic immunoglobulin-L-chain of
RT   subgroup IV of the kappa type (Bence-Jones protein Len).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN   [2]
RP   REVISION TO 9.
RA   Salomon A.;
RL   Submitted (AUG-1996) to Swiss-Prot.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PDB; 1EEQ; 01-FEB-01.
DR   PDB; 1EEU; 03-FEB-01.
DR   PDB; 1EFQ; 09-FEB-01.
DR   PDB; 1EK3; 06-MAR-01.
DR   PDB; 1LVE; 21-JAN-98.
DR   PDB; 3LVE; 18-MAY-99.
DR   PDB; 5LVE; 28-MAR-01.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN   1   23   FRAMEWORK-1.
FT   DOMAIN   24   40   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN   41   55   FRAMEWORK-2.
FT   DOMAIN   56   62   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN   63   94   FRAMEWORK-3.
FT   DOMAIN   95   101   COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN   102   113   FRAMEWORK-4.
FT   DISULFID 23   94   BY SIMILARITY.
FT   NON_TER 114   114
SQ   SEQUENCE   114 AA;   12640 MW;   0647F1D17F236485 CRC64;

Query Match   68.1%;   Score 383;   DB 1;   Length 114;
Best Local Similarity 65.5%;   Pred. No. 6.4e-34;
Matches   74;   Conservative 18;   Mismatches 15;   Indels 6;   Gaps 1;

```
Qy    1 NIVMTQSPKSMSVGERVTLTCKASENV------TYVSWYQQKPEQSPKLLIYGASNR 54
        :|||||||  :::  :|||:|:
Db    1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR 60

Qy   55 YTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        :||||||||::||||||||| ||
Db   61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGQGTKLEIK 113
```

RESULT 5
KV4C_HUMAN
ID   KV4C_HUMAN   STANDARD;   PRT;   134 AA.
AC   P06314;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-IV region B17 precursor.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041854; PubMed=2997713;
RA   Marsh P., Mills F., Gould H.;
RT   "Detection of a unique human V kappa IV germline gene by a cloned
RT   cDNA probe.";
RL   Nucleic Acids Res. 13:6531-6544(1985).
RN   [2]
RP   REVISION TO 76.
RA   Marsh P.;
RL   Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
CC
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; X02990; CAA26733.1; -.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   20
FT   CHAIN   21   134   IG KAPPA CHAIN V-IV REGION B17.
FT   DOMAIN   21   43   FRAMEWORK-1.
FT   DOMAIN   44   60   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN   61   75   FRAMEWORK-2.
FT   DOMAIN   76   82   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN   83   114   FRAMEWORK-3.
FT   DOMAIN   115   121   COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN   122   133   FRAMEWORK-4.
FT   DISULFID 43   114   BY SIMILARITY.
FT   NON_TER 134   134
SQ   SEQUENCE   134 AA;   14966 MW;   6413A22FD0738832 CRC64;

Query Match   66.9%;   Score 376;   DB 1;   Length 134;
Best Local Similarity 62.8%;   Pred. No. 4.3e-33;
Matches   71;   Conservative 21;   Mismatches 15;   Indels 6;   Gaps 1;

```
Qy    1 NIVMTQSPKSMSVGERVTLTCKASENV------TYVSWYQQKPEQSPKLLIYGASNR 54
        :|||||||  ::::|:||||:::||:::
Db   21 DIVMTQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLAWYQQKPGQPPKLLIYWASTR 80

Qy   55 YTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        :||||||||::||||||||| ||
Db   81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNLPWTFGQGTKVEIK 133
```

RESULT 6
KV1M_HUMAN
ID   KV1M_HUMAN   STANDARD;   PRT;   108 AA.

```
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Lay.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=7038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; K1HULY.
DR   HSSP; P01607; 1REI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  739993A95431434A CRC64;

Query Match             66.7%;  Score 375;  DB 1;  Length 108;
Best Local Similarity   65.4%;  Pred. No. 4.3e-33;
Matches   70;  Conservative   18;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
              :|||||||:|||||::|||||||:||||| |:|:::|||||||:|:|||||||||||||||
Db          1 DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60

Qy         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
              |:|||||||||||:|||||||||:|||||| |||||||||||:|:|:|
Db         61 RFSGSGSGTDFTFTISSLQPEDIATYYCCQYNNWPPTFGQGTKVEVK 107

RESULT 7
KV1Y_HUMAN
ID   KV1Y_HUMAN     STANDARD;     PRT;    108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Brunger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=8126384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS:This is a Bence-Jones protein.
DR   PDB; 1WTL; 01-NOV-94.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   CONFLICT     30     31       TN -> SD (IN REF. 2).
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       84     90
FT   STRAND       98     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;

Query Match             65.8%;  Score 370;  DB 1;  Length 108;
Best Local Similarity   63.6%;  Pred. No. 1.5e-32;
Matches   68;  Conservative   20;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
              :|||||||:|||||::|||||||:||||| |:|:|::|||||||:|:::|:||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60

Qy         61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
              |:||||||||||||||||:|::||:|||||| ||||||||||:|:||
Db         61 RFSGSGSGTDFTFTISSLQPEDIATYYCCQYDTLPLTFGGGTKVDIK 107

RESULT 8
KV1O_HUMAN
ID   KV1O_HUMAN     STANDARD;     PRT;    108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
```

```
Matches      67;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps     0;

Qy      1  NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD   60
              :|||||||| ||||||: || ||:|| |||||||::  |:::||||||||||||||||||||
Db      1  DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS   60

Qy     61  RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEI  106
              |:|||||| ||:| ||||:|:| ||:|:| |:|| |||||||||||
Db     61  RFSGSGSGTDYFTFTISSLQPEDIATYCCQQYQSLPYTFGQGTKLQI  106
```

RESULT 9
```
ID   KV1V_HUMAN              STANDARD;      PRT;    108 AA.
AC   P04430;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region BAN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86174817; PubMed=3083240;
RA   Dwulet F.E., O'Connor T.P., Benson M.D.;
RT   "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL   Mol. Immunol. 23:73-78(1986).
DR   PIR; A01878; KIHUBN.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Amyloid.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11840 MW;  CD3FD944FE96FD37 CRC64;
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Query Match   64.6%; Score 363; DB 1; Length 108;
Best Local Similarity   63.6%; Pred. No. 8.1e-32;
Matches   68; Conservative   17; Mismatches   22; Indels   0; Gaps   0;

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Qy      1  NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD   60
              :|||||||| ||||||: || ||:|| |||||||::  |:::||||||||||||||||||||
Db      1  DIQLTQSPSSLSASVGDRVTITCRASQSVYNYVANFQQKPGKAPKSLIYDASTLQSGVPS   60

Qy     61  RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK  107
              |:|||||| ||:| ||||:|:| ||:|:| |:|| ||||||||||:||
Db     61  NFTGSGSGTDFILTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIK  107
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RESULT 10
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ID   KV4B_HUMAN              STANDARD;      PRT;    133 AA.
AC   P06313;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-IV region JI precursor.
OS   Homo sapiens (Human).
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DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91663; KIHURE.
DR   PDB; 1REI; 17-FEB-84.
DR   PDB; 1AR2; 12-NOV-97.
DR   PDB; 1BWW; 29-DEC-99.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49       FRAMEWORK-2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88       FRAMEWORK-3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    107       FRAMEWORK-4.
FT   DISULFID     23     88
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       44     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   STRAND       60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   TURN         97     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;
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Query Match   64.9%; Score 365; DB 1; Length 108;
Best Local Similarity   63.2%; Pred. No. 5e-32;

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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041853; PubMed=2997712;
RA   Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA   Zachau H.G.;
RT   "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT   single germline gene.";
RL   Nucleic Acids Res. 13:6515-6529(1985).
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; Z00022; CAA77317.1; -.
DR   PIR; A01904; K4HUJI.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL         1     20
FT   CHAIN         21    133       IG KAPPA CHAIN V-IV REGION JI.
FT   DOMAIN        21    133       FRAMEWORK-1.
FT   DOMAIN        44     60       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        61     75       FRAMEWORK-2.
FT   DOMAIN        76     82       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        83    114       FRAMEWORK-3.
FT   DOMAIN       115    122       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       123    132       FRAMEWORK-4.
FT   DISULFID      43    114       BY SIMILARITY.
FT   NON_TER      133    133
SQ   SEQUENCE    133 AA;   14632 MW;  5FB3953066744AF4 CRC64;

Query Match             64.5%;  Score 362.5;  DB 1;  Length 133;
Best Local Similarity   63.7%;  Pred. No. 1.2e-31;
Matches   72;  Conservative   19;  Mismatches   19;  Indels   15;  Gaps   2;

Qy      1  NIVMTQSPKSMSMSVGERVTLTCKASENVV------TYVSWYQQKPEQSPKLLIYGASNR   54
           :||||||  ||:|||:||::|::        |||||||||||||||||||||
Db     21  DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR   80

Qy     55  YTGVPDRPTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK  107
           ||||||  ||||||:|||||||||||||| || |||||||||||||:|||
Db     81  ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDTIP-TFGGGTKVEIK  132


RESULT 11
KVLH_HUMAN
ID   KVLH_HUMAN       STANDARD;      PRT;   108 AA.
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Hau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
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```
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT   subgroups.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01868; KlHUHU.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN         1     23       FRAMEWORK-1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        35     49       FRAMEWORK-2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        57     88       FRAMEWORK-3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN        98    107       FRAMEWORK-4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;   11671 MW;  08D3A6160D8D0618 CRC64;

Query Match             63.9%;  Score 359;  DB 1;  Length 108;
Best Local Similarity   61.7%;  Pred. No. 2.2e-31;
Matches   66;  Conservative   22;  Mismatches   19;  Indels   0;  Gaps   0;

Qy      1  NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD   60
           :|:||||| :|: :|||||||:|||::::| |||||||:::|||::  :||::||  ||
Db      1  DIQMTQSPSSLSASVGDRVTITCRASQSISSYLSWYQQKPGKAPQVLIYAASSLPSGVPS   60

Qy     61  RPTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK  107
           | :||||| ||||||||::|||| |||||| ||| : :|||||:|||
Db     61  RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITPTSFGQGTRVEIK  107


RESULT 12
KV3J_MOUSE
ID   KV3J_MOUSE       STANDARD;      PRT;   111 AA.
AC   P01662;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region ABPC 22/PC 9245.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE (ABPC 22).
RX   MEDLINE=79012520; PubMed=99744;
RA   McKean D.J., Bell M., Potter M.;
RT   "Mechanisms of antibody diversity: multiple genes encode structurally
RT   related mouse kappa variable regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN   [2]
RP   SEQUENCE (PC 9245).
RX   MEDLINE=79073152; PubMed=103003;
RA   Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT   "Rearrangement of genetic information may produce immunoglobulin
RT   diversity.";
RL   Nature 276:785-790(1978).
CC   -!- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
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FT   DOMAIN                          79        110                  FRAMEWORK-3.
FT   DOMAIN                         111        119                  COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN                         120        129                  FRAMEWORK-4.
FT   DISULFID                        45        110                  BY SIMILARITY.
FT   NON_TER                        129        129
SQ   SEQUENCE      129 AA;    14235 MW;   CAF076BC7E5574C8 CRC64;

Query Match             63.9%;  Score 359;  DB 1;  Length 129;
Best Local Similarity   59.8%;  Pred. No. 2.7e-31;
Matches   64;  Conservative   19;  Mismatches   24;  Indels    0;  Gaps    0;

Qy     1  NIVMTQSPKSMSMSVGERVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD  60
          ::|||||||||||||||:|||||::::|||||||:: :::||||||| :::||||||||||
Db    23  DIQMTQSPSSLSASVGDRVTITCRAGHNITNFLSWYQQKPGKAPTLLIYAVSNLQVGVPS  82

Qy    61  RFTGGGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK  107
          |||||||||||||||||| :::|||||||||||||||||||||||
Db    83  RFSGSGSGAEFTLTIISSLQPEDFATYYCQQYNFSFTFGGGTKVDNK  129


RESULT 14
KV1L_HUMAN
ID   KV1L_HUMAN     STANDARD;      PRT;    108 AA.
AC   P01604;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Kue.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79237924; PubMed=112021;
RA   Eulitz M., Kley H.P., Zeitler H.-J.;
RT   "The primary structure of the Bence-Jones protein Kue. The amino acid
RT   sequence of the variable part of a human L-chain of the kappa-type.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC   -!- MISCELLANEOUS: THIS IS THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A Bence-Jones protein.
DR   PIR; A01870; KIHUKU.
DR   HSSP; P01607; IREI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN                           1        23                  FRAMEWORK-1.
FT   DOMAIN                          24        34                  COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN                          35        49                  FRAMEWORK-2.
FT   DOMAIN                          50        56                  COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN                          57        88                  FRAMEWORK-3.
FT   DOMAIN                          89        97                  COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN                          98       107                  FRAMEWORK-4.
FT   DISULFID                        23        88                  BY SIMILARITY.
FT   NON_TER                        108       108
SQ   SEQUENCE      108 AA;    12127 MW;   906679A5D90B4E98 CRC64;

Query Match             63.7%;  Score 358;  DB 1;  Length 108;
Best Local Similarity   61.7%;  Pred. No. 2.8e-31;
Matches   66;  Conservative   20;  Mismatches   21;  Indels    0;  Gaps    0;

Qy     1  NIVMTQSPKSMSMSVGERVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD  60
          ::|||||||||:|||::: :::|||||||:: :::||||||| :::||||||||::||||
Db     1  DIQMTQSPSTQPASVGDRVTITCRASQSIN:WLAWYQQKPEKAPKLIYKASTLETGVPS  60

Qy    61  RFTGGGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK  107
          |||||||||||||||||| :::|||||||||||||||||||||||
```

```
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN                           1        23                  FRAMEWORK-1.
FT   DOMAIN                          24        38                  COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN                          39        53                  FRAMEWORK-2.
FT   DOMAIN                          54        60                  COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN                          61        92                  FRAMEWORK-3.
FT   DOMAIN                          93       101                  COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN                         102       111                  FRAMEWORK-4.
FT   DISULFID                        23        92                  BY SIMILARITY.
FT   NON_TER                        111       111
SQ   SEQUENCE      111 AA;    12041 MW;   D7DF0609303453CE CRC64;

Query Match             63.9%;  Score 359;  DB 1;  Length 111;
Best Local Similarity   63.1%;  Pred. No. 2.2e-31;
Matches   70;  Conservative   17;  Mismatches   20;  Indels    4;  Gaps    1;

Qy     1  NIVMTQSPKSMSMSVGERVLTCKASENVVTY----VSWYQQKPEQSPKLLIYGASNRYT  56
          ::|||||||||||||||:|||||:  ::::||||||:: :::||||||||||||
Db     1  NIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNLES  60

Qy    57  GVPDRFTGGGSATDFLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK  107
          ||| |||||||||||:||||:||||||||||||:||||||||||||||||
Db    61  GVPARFSGSGSGSRTDFTLTIDDVEADDAATYYCQQNNEDPYTFGGGTKLEIK  111


RESULT 13
KV1X_HUMAN
ID   KV1X_HUMAN     STANDARD;      PRT;    129 AA.
AC   P04432;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Daudi precursor.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X00966; CAA25478.1; ALT_TERM.
DR   PIR; A01884; K1HUDI.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL                           1        22
FT   CHAIN                           23       129                  IG KAPPA CHAIN V-I REGION DAUDI.
FT   DOMAIN                          23        45                  FRAMEWORK-1.
FT   DOMAIN                          46        56                  COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN                          57        71                  FRAMEWORK-2.
FT   DOMAIN                          72        78                  COMPLEMENTARITY-DETERMINING-2.
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Db   61 RFSGSGSGTEFTLTINSLQPDDFATYCQQYSRYPYTFGQGTKLDIK 107

RESULT 15
KV3H_MOUSE
ID   KV3H_MOUSE   STANDARD;   PRT;   111 AA.
AC   P01660;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region PC 3741/TEPC 111.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE (PC 3741).
RX   MEDLINE=79073152; PubMed=103003;
RA   Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT   "Rearrangement of genetic information may produce immunoglobulin
RT   diversity.";
RL   Nature 276:785-790(1978).
RN   [2]
RP   SEQUENCE (TEPC 111).
RX   MEDLINE=79012520; PubMed=99744;
RA   McKean D.J., Bell M., Potter M.;
RT   "Mechanisms of antibody diversity: multiple genes encode structurally
RT   related mouse kappa variable regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC   -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR   PIR; A93204; KVMS37.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN   1   23   FRAMEWORK-1.
FT   DOMAIN   24   38   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN   39   53   FRAMEWORK-2.
FT   DOMAIN   54   60   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN   61   92   FRAMEWORK-3.
FT   DOMAIN   93   101   COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN   102   111   FRAMEWORK-4.
FT   DISULFID   23   92   BY SIMILARITY.
FT   NON_TER   111   111
SQ   SEQUENCE   111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match   63.7%; Score 358; DB 1; Length 111;
Best Local Similarity   61.3%; Pred. No. 2.9e-31;
Matches   68; Conservative   21; Mismatches   18; Indels   4; Gaps   1;

Qy   1 NIVMTQSPKSMSMSVGERVLTCKASENVVTY----VSWYQQKPEQSPKLLIYGASNRYT 56
        :|:|||:||| :|||||:|||| |:||:|:| : |:|||||:|| |||||| :
Db   1 DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLES 60

Qy   57 GVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
        |:|:|||||||| |||||||:| |||||:|:|:| ||||||||||||||:|
Db   61 GIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPYTFGGGTKLEIK 111

Search completed: August 16, 2004, 11:08:35
Job time : 7.67713 secs

```
                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     August 16, 2004, 11:08:06 ; Search time 31.6682 Seconds
                                   (without alignments)
                              1066.069 Million cell updates/sec

Title:           US-09-889-300A-2
Perfect score:   562
Sequence:        1 NIVMTQSPKSMSMSVGERVT..........CGQGYSYPYTFGGGTKLEIK 107

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1017041 segs, 31551820 residues

Total number of hits satisfying chosen parameters:      1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_25:*
           1: sp_archea:*
           2: sp_bacteria:*
           3: sp_fungi:*
           4: sp_human:*
           5: sp_invertebrate:*
           6: sp_mammal:*
           7: sp_mhc:*
           8: sp_organelle:*
           9: sp_phage:*
          10: sp_plant:*
          11: sp_rodent:*
          12: sp_virus:*
          13: sp_vertebrate:*
          14: sp_unclassified:*
          15: sp_rvirus:*
          16: sp_bacteriap:*
          17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
Result         Query
No.    Score   Match  Length  DB  ID       Description
----   -----   -----  ------  --  --       -----------
  1     406    72.2    108    11  Q8VIJ0   Q8vij0 mus musculu
  2     378    67.3     99    11  Q9JL74   Q9jl74 mus musculu
  3     370.5  65.9    107     4  Q96SA9   Q96sa9 homo sapien
  4     369    65.7    108     4  Q9UL77   Q9ul77 homo sapien
  5     366.5  65.2    109     4  Q9UL78   Q9ul78 homo sapien
  6     366    65.1    107    11  Q9ERZ9   Q9erz9 mus musculu
  7     363.5  64.7    109     4  Q9UL85   Q9ul85 homo sapien
  8     363.5  64.7    238    11  Q99M37   Q99m37 mus musculu
  9     358    63.7    234     4  Q7Z473   Q7z473 homo sapien
 10     357    63.5    108     4  Q9UL79   Q9ul79 homo sapien
 11     357    63.5    236     4  Q7Z3Y4   Q7z3y4 homo sapien
 12     354    63.0    108     4  Q9UL70   Q9ul70 homo sapien
 13     351.5  62.5    107     4  Q9UL81   Q9ul81 homo sapien.
 14     350.5  62.4    238    11  Q8VCl6   Q8vci6 mus musculu
 15     347.5  61.8    239    11  Q8VC55   Q8vc55 mus musculu
 16     347    61.7    108     4  Q9UL83   Q9ul83 homo sapien
 17     347    61.7    236    11  Q7TMK3   Q7tmk3 mus musculu
 18     346.5  61.7    112    11  Q8K1F3   Q8k1f3 mus musculu
 19     345    61.4    111    11  Q920E9   Q920e9 mus musculu
 20     342.5  60.9    114    11  Q8K1F1   Q8k1f1 mus musculu
 21     342    60.9    236    11  Q7TS98   Q7ts98 mus musculu
 22     339.5  60.4    109     4  Q9UL86   Q9ul86 homo sapien
 23     338    60.1    214    11  Q9R1A5   Q9r1a5 mus musculu
 24     337    60.0    234    11  Q91WF8   Q91wf8 mus musculu
 25     336.5  59.9    134    11  Q8VDD0   Q8vdd0 mus musculu
 26     335    59.6    237    13  Q7SZ36   Q7sz36 xenopus lae
 27     333    59.3    111    11  Q811U6   Q811u6 mus musculu
 28     332    59.1    109    11  Q920E6   Q920e6 mus musculu
 29     331.5  59.0    112    11  Q8K1F2   Q8k1f2 mus musculu
 30     331    58.9    298    11  Q9QYF0   Q9qyf0 mus musculu
 31     330    58.7    116     4  Q96PF6   Q96pf6 homo sapien
 32     329.5  58.6    104    11  Q9JL82   Q9jl82 mus musculu
 33     329.5  58.6    243    11  Q7TQM2   Q7tqm2 mus musculu
 34     329    58.5    233    11  Q91WS9   Q91ws9 mus musculu
 35     328.5  58.5    106     5  Q9U410   Q9u410 schistosoma
 36     326.5  58.1    239     4  Q8NEK0   Q8nek0 homo sapien
 37     325    57.8    234    11  Q8R062   Q8r062 mus musculu
 38     324.5  57.7    239     4  Q8TCD0   Q8tcd0 homo sapien
 39     321    57.5    234    11  Q8VCP0   Q8vcp0 mus musculu
 40     321    57.1    131    11  Q811C3   Q811c3 mus musculu
 41     316.5  56.3    235    11  Q7TMK0   Q7tmk0 mus musculu
 42     313    55.7    109     6  Q9N0W5   Q9n0w5 oryctolagus
 43     313    55.7    114     4  Q9UL80   Q9ul80 homo sapien
 44     311.5  55.4    239    11  Q8K0F8   Q8k0f8 mus musculu
 45     309    55.0    101    11  Q9JL78   Q9jl78 mus musculu
```

ALIGNMENTS

```
RESULT 1
Q8VIJ0
ID   Q8VIJ0;        PRELIMINARY;       PRT;      108 AA.
AC   Q8VIJ0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-DNA light chain (Fragment).
GN   VK19.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H/HeJ-lpr/lpr;
RX   MEDLINE=96409289; PubMed=8814271;
RA   Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT   "Differences in V kappa gene utilization and VH CDR3 sequence among
RT   anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL   Eur. J. Immunol. 26:2225-2233(1996).
DR   EMBL; U59155; AAB02917.1; -.
DR   PIR; A33933; A33933.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1
FT   NON_TER     108      108
SQ   SEQUENCE    108 AA;   11859 MW;   68506D75613DBFBE CRC64;

     Query Match             72.2%;   Score 406;  DB 11;  Length 108;
     Best Local Similarity   74.8%;   Pred. No. 2.6e-36;
     Matches    80;  Conservative   10;  Mismatches  17;  Indels    0;  Gaps    0;

Qy     1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
           :|||||||||||||||||||| |:|||||:|:|:|||||| :||:||:|||:|||: :||
Db     1 DIVMTQSQTFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKALITSASYPYSGVPH 60
```

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Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          |:||||| |||||||||||||                  ||||||||||
Db   61 RFSGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPYTFGGGTKLEIK 107


RESULT 2
Q9JL74
ID   Q9JL74       PRELIMINARY;     PRT;    99 AA.
AC   Q9JL74;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-myosin immunoglobulin light chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=20448942; PubMed=10992488;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206032; AAF69330.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER    1      1
FT   NON_TER    99     99
SQ   SEQUENCE   99 AA;  10939 MW;  3B25D0E784533324 CRC64;

Query Match             67.3%;
Best Local Similarity   74.7%;   Score 378; DB 11; Length 99;
Matches   74;  Conservative    8;  Pred. No. 2.5e-33; Mismatches   17;  Indels    0;  Gaps    0;

Qy    9 KSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSA 68
          |::::|:||||||||||||||  :|||||||||||||||||||||||||||||
Db    1 KFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGGSPKLLIYYASNRYTGVPDRFTGSGYG 60

Qy   69 TDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          |||||||||||||||                 ||||||||||||
Db   61 TDFTFTISTVQAEDLAVYFCQQDYSSPRTFGGGTKLEIK 99


RESULT 3
Q96SA9
ID   Q96SA9       PRELIMINARY;     PRT;   107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE   variable region (Fragment).
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9837593; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
RL   J. Immunol. 161:2020-2031(1998).
```

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DR   EMBL; U96396; AAB68785.1; -.
DR   PIR; B49047; B49047.
DR   PIR; S34083; S34083.
DR   PIR; S34086; S34086.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER    1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;  11520 MW;  4B43E9C5B577F16 CRC64;

Query Match             65.9%;
Best Local Similarity   65.4%;   Score 370.5;  DB 4;  Length 107;
Matches   70;  Conservative   19;  Pred. No. 1.8e-32;  Mismatches   17;  Indels    1;  Gaps    1;

Qy    1 NIVMTQSPKSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          :|::||||||::|||||||||||:|::::|||||||||::|:||||||||| :|||
Db    1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          |:||||| ||||||||||||| ::|||||||:||::|||||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYS-TLTFGGGTKVEIK 106


RESULT 4
Q9UL77
ID   Q9UL77       PRELIMINARY;     PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.,
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.",
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035037; AAD56273.1; -.
DR   PIR; B49047; B49047.
DR   PIR; S34083; S34083.
DR   HSSP; P01607; IREI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER    1      1
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  11738 MW;  C0668176C4D16F3 CRC64;

Query Match             65.7%;
Best Local Similarity   63.6%;   Score 369;  Pred. No. 2.7e-32;  DB 4;  Length 108;
Matches   68;  Conservative   20;  Mismatches   19;  Indels    0;  Gaps    0;

Qy    1 NIVMTQSPKSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          :|::||||||::|||||||||||:|::::|||||||||::|:||||||||| :|||
Db    1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          |:||||| ||||||||||||| ::|||||||:||::|||||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
```

RESULT 5
Q9UL78
ID   Q9UL78   PRELIMINARY;   PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035036; AAD56272.1; -.
DR   PIR; A30601; A30601.
DR   PIR; A30608; A30608.
DR   PIR; A30608; A30608.
DR   PIR; B30601; B30601.
DR   PIR; B30607; B30607.
DR   PIR; B30607; B30607.
DR   PIR; C30601; C30601.
DR   PIR; C30607; C30607.
DR   PIR; C30608; C30608.
DR   PIR; D30601; D30601.
DR   PIR; D30607; D30607.
DR   PIR; D30607; D30607.
DR   PIR; D30608; D30608.
DR   PIR; F30607; F30607.
DR   PIR; F30608; F30608.
DR   PIR; G30601; G30601.
DR   PIR; G30608; G30608.
DR   PIR; G30608; G30608.
DR   PIR; H30607; H30607.
DR   PIR; H30608; H30608.
DR   PIR; I30601; I30601.
DR   PIR; PH0963; PH0963.
DR   PIR; PH0965; PH0965.
DR   PIR; S34096; S34096.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   109   109
SQ   SEQUENCE   109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match
Best Local Similarity   65.2%; Score 366.5; DB 4; Length 109;
Matches   70; Conservative   20; Mismatches 16; Indels   1; Gaps   1;

Qy   2 IVMTQSPKSMSMSVGERVTLTCKASENV-VTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

Db   2 IVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPD 61

Qy   61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSPYTFGGGTKLEIK 107

Db   62 RFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108

RESULT 6
Q9ERZ9
ID   Q9ERZ9   PRELIMINARY;   PRT;   107 AA.
AC   Q9ERZ9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti human TNF-alpha light chain variable region (Fragment).

OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT   "Cloning and sequencing of the light chain fragment of variable region
RT   genes of an anti-hTNF-a monoclonal antibody.";
RL   J. Cell. Mol. Immunol. 12:21-26(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT   "Construction and sequencing of the single-chain antibody gene of a
RT   human TNF-alpha specific monoclonal antibody.";
RL   Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF262753; AAG23804.1; -.
DR   PDB; 2AP2; 24-NOV-99.
DR   PDB; 43C9; 24-JUL-02.
DR   PDB; 43CA; 24-JUL-02.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   107   107
SQ   SEQUENCE   107 AA; 11784 MW; 2B1EEA6604A2C3 CRC64;

Query Match
Best Local Similarity   65.1%; Score 366; DB 11; Length 107;
Matches   69; Conservative   17; Mismatches 15; Indels   6; Gaps   1;

Qy   4 MTQSPKSMSMSVGERVTLTCKASENV------TYVSWYQQKPEQSPKLLIYGASNRYTG 57

Db   1 MTQSPSSLAMSVGQKVTMSCKSSQSVLNSNTQKNYLAWYQKKPGQSPELLVYFASTRESG 60

Qy   58 VPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSPYTFGGGTKL 104

Db   61 VPDRFMGSGSGTDFTLTISSVQTEDLADYFCQQHYRTPFTFGSGTKL 107

RESULT 7
Q9UL85
ID   Q9UL85   PRELIMINARY;   PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035029; AAD56265.1; -.
DR   PIR; D30609; D30609.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.

```
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    109    109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1B43E7C7AFACCC CRC64;

Query Match      64.7%;  Score 363.5;  DB 4;  Length 109;
Best Local Similarity   65.4%;  Pred. No. 1.1e-31;
Matches  70;  Conservative  19;  Mismatches  17;  Indels   1;  Gaps   1;

Qy     2 IVMTQSPKSMSMSVGERVTLTCKASENVTVSWYQQKPEQSPKLLIYGASNRYTGVPDR 61
           |||||| :::::||| ||| ||::: ::||||  :||||||||||||:|:||:||::|
Db     2 IVNTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPAR 61

Qy    62 FTGSGSATDFTLTISSVQAEDLADYHCGQGYSY-PYTFGGGTKLEIK 107
           |:||:||  || |||||||||||||| :|| ||| |||||||||||
Db    62 FSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIK 108

RESULT 8
Q99M37
ID   Q99M37       PRELIMINARY;       PRT;   238 AA.
AC   Q99M37;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002035; AAH02035.1; -.
DR   PIR; A31807; A31807.
DR   PIR; A32248; A32248.
DR   PIR; B32248; B32248.
DR   PIR; C32248; C32248.
DR   PIR; F32530; F32530.
DR   PIR; PH1042; PH1042.
DR   PIR; PH1043; PH1043.
DR   PIR; PH1044; PH1044.
DR   PIR; S07455; S07455.
DR   PIR; S16112; S16112.
DR   PIR; S24500; S24500.
DR   PIR; S24501; S24501.
DR   PIR; S24503; S24503.
DR   PIR; S24504; S24504.
DR   PIR; S24529; S24529.
DR   PIR; S24532; S24532.
DR   PIR; S24533; S24533.
DR   PIR; S24535; S24535.
DR   PIR; S24536; S24536.
DR   PIR; S24538; S24538.
DR   PDB; 1I9I; 25-DEC-02.
DR   PDB; 1LO2; 31-JUL-02.
DR   PDB; 1LO3; 31-JUL-02.
DR   PDB; 1LO4; 31-JUL-02.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   238 AA;  26344 MW;  FB2B06A0B801330A CRC64;

Query Match      64.7%;  Score 363.5;  DB 11;  Length 238;
Best Local Similarity   59.8%;  Pred. No. 2.9e-31;
Matches  67;  Conservative  22;  Mismatches  18;  Indels   5;  Gaps   1;

Qy     1 NIVMTQSPKSMSMSVGERVTLTCKASENVV----TVSWYQQKPEQSPKLLIYGASNRY 55
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Db    20 DVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79
             ::|||| ||| || || :|  :|  || :| :  |||||||||||||
Qy    56 TGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
             ||||||:||||||||||||| :| ||| |||||||||||
Db    80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVVYCFQSHVPTFGSGTKLEIK 131

RESULT 9
Q72473
ID   Q72473       PRELIMINARY;       PRT;   234 AA.
AC   Q72473;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056256; AAH56256.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25674 MW;  1A2C259BAB51BC0F CRC64;

Query Match      63.7%;  Score 358;  DB 4;  Length 234;
Best Local Similarity   61.3%;  Pred. No. 1.1e-30;
Matches  65;  Conservative  21;  Mismatches  20;  Indels   0;  Gaps   0;

Qy     2 IVMTQSPKSMSMSVGERVTLTCKASENVTVSWYQQKPEQSPKLLIYGASNRYTGVPDR 61
Db    22 IRMTQSPSSFSASTGDRVTIICRASQSIGSYLAWYQQKPGKAPQLLIYAASTLQSGVPSR 81

Qy    62 FTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
Db    82 FSGSASGTDFTLSISCLQSEDFATYCQQYTYPWTFGQGTKVEIK 127

RESULT 10
Q9UL79
ID   Q9UL79       PRELIMINARY;       PRT;   108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```

```
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035035; AAD56271.1; -.
DR   PIR; S23638; S23638.
     HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;   11787 MW;   DB5845F19724FB4E CRC64;

Query Match             63.5%;  Score 357;  DB 4;  Length 108;
Best Local Similarity   60.7%;  Pred. No. 5.4e-31;
Matches   65;  Conservative   21;  Mismatches   21;  Indels    0;  Gaps    0;

Qy      1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          : ||||||:||:|||||||:::|: :.:||||||||| ::|:|||| ::|||| |||||||
Db      1 DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS 60

Qy     61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          |:||||| |||||||||| :|:|| |||||| |:|:| |||||||||
Db     61 RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK 107


RESULT 11
Q7Z3Y4
ID   Q7Z3Y4      PRELIMINARY;     PRT;   236 AA.
AC   Q7Z3Y4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
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RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005332; AAH05332.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;   25702 MW;   7FBFE4ED23084BC6 CRC64;

Query Match             63.5%;  Score 357;  DB 4;  Length 236;
Best Local Similarity   62.6%;  Pred. No. 1.5e-30;
Matches   67;  Conservative   19;  Mismatches   21;  Indels    0;  Gaps    0;

Qy      1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          : ||||||:||:|||||||:::|: :.:||||||||| ::|:|||| ::|||| |||||||
Db     23 DIQMTQSPSSLSASVGDTVTITCRASQDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82

Qy     61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          :|:||| |||||||||| :|:|| |||||| |:|:| |||||||||
Db     83 KFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIK 129


RESULT 12
Q9UL70
ID   Q9UL70      PRELIMINARY;     PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035044; AAD56280.1; -.
DR   PIR; PH0863; PH0863.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;   11633 MW;   B7BEDC3E41FCCA37 CRC64;

Query Match             63.0%;  Score 354;  DB 4;  Length 108;
Best Local Similarity   63.6%;  Pred. No. 1.1e-30;
Matches   68;  Conservative   16;  Mismatches   23;  Indels    0;  Gaps    0;

Qy      1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPD 60
          : ||||||:||:|||||||:::|: :.:||||||||| ::|:|||| ::||||:|||||||
Db      1 DIQMTQSPSSLSASVGDRVTITCRASQGISNVLAWYQQKPGKVPKSLIYAASTLQSGVPS 60

Qy     61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          ||:||||| |||||||||| :|:|| |||||| |:|:| |||||||||
Db     61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107


RESULT 13
Q9UL81
ID   Q9UL81      PRELIMINARY;     PRT;   107 AA.
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AC    Q9UL81;
DT    01-MAY-2000 (TrEMBLrel. 13, Created)
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Myosin-reactive immunoglobulin light chain variable region
DE    (Fragment).
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=9827139; PubMed=9614934;
RA    Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA    Young D.C.;
RT    "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT    fetus.";
RL    Clin. Immunol. Immunopathol. 87:184-192(1998).
DR    EMBL; AF035033; AAD56269.1; -.
DR    HSSP; P01607; 1REI.
DR    InterPro; IPR007110; Ig-like.
DR    InterPro; IPR003596; Ig_v.
DR    Pfam; PF00047; ig; 1.
DR    SMART; SM00406; IGv; 1.
DR    PROSITE; PS50835; IG_LIKE; 1.
FT    NON_TER       1      1
FT    NON_TER     107    107
SQ    SEQUENCE   107 AA;  11501 MW;  070549FDE0754748 CRC64;

Query Match             62.5%;  Score 351.5;  DB 4;  Length 107;
Best Local Similarity   61.7%;  Pred. No. 2.1e-30;
Matches   66;  Conservative   20;  Mismatches   20;  Indels    1;  Gaps    1;

Qy      1 NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRY 60
          ||||||||||||||||:||:||||||||:||||:|||||||||||||||||::||
Db      1 DIQMTQSPSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy     61 RFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          ||:||||:||||||||:||:||||||||||| |:||||||||||||
Db     61 RFSGSGSGTDFTLTISGLQAEDFATYYCQQSYS-ALTFGPGTKVDIR 106

RESULT 14
Q8VCI6;
ID    Q8VCI6;             PRELIMINARY;       PRT;     238 AA.
AC    Q8VCI6;
DT    01-MAR-2002 (TrEMBLrel. 20, Created)
DT    01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Hypothetical protein.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Colon;
RA    Strausberg R.;
RL    Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; BC019760; AAH19760.1; -.
DR    PIR; A27887; A27887.
DR    PIR; A32248; A32248.
DR    PIR; A33933; A33933.
DR    PIR; B27887; B27887.
DR    PIR; B30577; B30577.
DR    PIR; B31485; B31485.
DR    PIR; B32248; B32248.
DR    PIR; B41940; B41940.
DR    PIR; C27887; C27887.
DR    PIR; C32248; C32248.
DR    PIR; C34904; C34904.
DR    PIR; D27887; D27887.
DR    PIR; D29380; D29380.

DR    PIR; E28833; E28833.
DR    PIR; F32530; F32530.
DR    PIR; H31485; H31485.
DR    PIR; PH0106; PH0106.
DR    PIR; PH1030; PH1030.
DR    PIR; PH1031; PH1031.
DR    PIR; PH1034; PH1034.
DR    PIR; PL0257; PL0257.
DR    PIR; PT0359; PT0359.
DR    PIR; S07455; S07455.
DR    PIR; S16112; S16112.
DR    PIR; S26334; S26334.
DR    PIR; S53750; S53750.
DR    PIR; S60066; S60066.
DR    InterPro; IPR007110; Ig-like.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_v.
DR    Pfam; PF00047; ig; 2.
DR    SMART; SM00406; IGv; 1.
DR    PROSITE; PS50835; IG_LIKE; 2.
DR    PROSITE; PS00290; IG_MHC; 1.
KW    Hypothetical protein.
SQ    SEQUENCE   238 AA;  26224 MW;  35EC08E3DE5414AD CRC64;

Query Match             62.4%;  Score 350.5;  DB 11;  Length 238;
Best Local Similarity   58.9%;  Pred. No. 7.5e-30;
Matches   66;  Conservative   21;  Mismatches   20;  Indels    5;  Gaps    1;

Qy      1 NIVMTQSPKSMSMSVGERVTLTCKASENVV----TYVSWYQQKPEQSPKLLIYGASNRY 55
          :||||:||||||||||||||||||||:||:::|:::  |||||||||||||||||||||
Db     20 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 79

Qy     56 TGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          :||||||:||||||||||||||:||||||||||||||||||||||||||||
Db     80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPFTFGGGTKLEIK 131

RESULT 15
Q8VC55;
ID    Q8VC55;             PRELIMINARY;       PRT;     239 AA.
AC    Q8VC55;
DT    01-MAR-2002 (TrEMBLrel. 20, Created)
DT    01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE    Hypothetical protein.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Colon;
RA    Strausberg R.;
RL    Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; BC021781; AAH21781.1; -.
DR    PIR; A33933; A33933.
DR    PDB; 1KC5; 24-JUL-02.
DR    GO; GO:0005576; C:extracellular; IEA.
DR    GO; GO:0015070; F:toxin activity; IEA.
DR    GO; GO:0009405; P:pathogenesis; IEA.
DR    InterPro; IPR004214; Conotoxin.
DR    InterPro; IPR007110; Ig-like.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_v.
DR    Pfam; PF02950; Conotoxin; 1.
DR    Pfam; PF00047; ig; 2.
DR    SMART; SM00406; IGv; 1.
DR    PROSITE; PS50835; IG_LIKE; 2.
DR    PROSITE; PS00290; IG_MHC; 1.
KW    Hypothetical protein.
SQ    SEQUENCE   239 AA;  26303 MW;  C16119CACA25C337 CRC64;

Query Match             61.8%;  Score 347.5;  DB 11;  Length 239;
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Best Local Similarity 56.2%; Pred. No. 1.6e-29;
Matches 63; Conservative 26; Mismatches 18; Indels 5; Gaps 1;

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Qy    1 NIVMTQSPKSMSMSVGERVTLTCKASENVV-----TYVSWYQQKPEQSPKLLIYGASNRY 55
          ::|::|::||:|  ::||::::::|:::::      ||:  |||:|||::||||||||:
Db   21 DVVLTQTPLSLPVNIGDQASISCKSTKSLLNSDGFTYLDWYLQKPGQSPQLLIYLVSNRF 80

Qy   56 TGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 107
          :||||||||||||:||||||:|  |:|:||:||    ||:||||||||||||
Db   81 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSNHLPYTFGGGTKLEIK 132
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Search completed: August 16, 2004, 11:10:29
Job time : 31.6682 secs

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     August 16, 2004, 11:08:07 ; Search time 15.0852 Seconds
                                        (without alignments)
                                        396.986 Million cell updates/sec

Title:      US-09-889-300A-1
Perfect score:  614
Sequence:   1 QVQLQQSGAELVRPGTSVKV.........ARDGPWFAYWGQGTLVTVSA 116

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:   389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:   389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued Patents AA:*
            1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
            2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
            3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
            4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
            5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
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Result No.	Score	% Match Score	Query Length	DB	ID	Description
1	554.5	90.3	119	1	US-08-458-516-11	Sequence 11, Appl
2	554.5	90.3	138	1	US-08-458-516-7	Sequence 7, Appli
3	546.5	89.0	119	3	US-08-767-128-10	Sequence 10, Appl
4	510.5	83.1	138	3	US-08-589-939-1	Sequence 1, Appli
5	503.5	82.0	119	1	US-08-458-516-10	Sequence 10, Appl
6	503.5	82.0	222	1	US-08-458-516-22	Sequence 22, Appl
7	503.5	82.0	235	1	US-08-458-516-23	Sequence 23, Appl
8	503.5	82.0	449	1	US-08-458-516-13	Sequence 13, Appl
9	497.5	81.0	117	3	US-09-157-370-2	Sequence 2, Appli
10	490.5	79.9	119	3	US-08-767-128-20	Sequence 20, Appl
11	485.5	79.1	121	3	US-08-881-037-65	Sequence 65, Appl
12	482.5	78.6	119	2	US-08-737-560A-10	Sequence 10, Appl
13	482	78.5	122	2	US-07-916-098A-10	Sequence 10, Appl
14	481.5	78.4	119	4	US-09-438-954-39	Sequence 39, Appl
15	480	78.2	137	1	US-08-392-419-2	Sequence 2, Appli
16	478.5	77.9	123	1	US-08-497-312-15	Sequence 15, Appl
17	478.5	77.9	123	2	US-08-560-558E-28	Sequence 28, Appl
18	478	77.9	120	1	US-08-397-411-11	Sequence 11, Appl
19	478	77.9	122	1	US-08-236-520-9	Sequence 9, Appli
20	478	77.9	122	5	PCT-US95-05262-9	Sequence 9, Appli
21	478	77.9	139	2	US-08-556-586-4	Sequence 4, Appli
22	477	77.7	116	1	US-07-634-278-3	Sequence 3, Appli
23	477	77.7	116	1	US-07-634-278-14	Sequence 14, Appl
24	477	77.7	116	1	US-08-477-728-3	Sequence 3, Appli
25	477	77.7	116	1	US-08-477-728-14	Sequence 14, Appl
26	477	77.7	116	1	US-08-474-040-3	Sequence 3, Appli
27	477	77.7	116	1	US-08-474-040-14	Sequence 14, Appl

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28   477   77.7   116   1   US-08-487-200-3       Sequence 3, Appli
29   477   77.7   116   1   US-08-487-200-14      Sequence 14, Appl
30   477   77.7   116   1   US-08-488-113B-167    Sequence 167, App
31   477   77.7   116   1   US-08-477-484B-167    Sequence 167, App
32   477   77.7   116   1   US-08-107-669D-53     Sequence 53, Appl
33   477   77.7   116   1   US-08-472-788A-85     Sequence 85, Appl
34   477   77.7   116   2   US-08-477-531B-53     Sequence 53, Appl
35   477   77.7   116   2   US-08-646-360-167     Sequence 167, App
36   477   77.7   116   2   US-08-082-842A-85     Sequence 85, Appl
37   477   77.7   116   3   US-08-839-765-167     Sequence 167, App
38   477   77.7   116   3   US-09-136-389-167     Sequence 167, App
39   477   77.7   116   3   US-08-484-537-3       Sequence 3, Appli
40   477   77.7   116   3   US-08-484-537-14      Sequence 14, Appl
41   477   77.7   116   4   US-09-610-838-167     Sequence 167, App
42   477   77.7   116   4   US-09-711-485-167     Sequence 167, App
43   477   77.7   118   2   US-08-428-257A-74     Sequence 74, Appl
44   477   77.7   118   3   US-07-987-264-14      Sequence 14, Appl
45   477   77.7   239   3   US-08-279-772A-8      Sequence 8, Appli
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                        ALIGNMENTS

RESULT 1
US-08-458-516-11
; Sequence 11, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
;  APPLICANT:  Co, Man Sung
;  APPLICANT:  Tso, J. Yun
;  TITLE OF INVENTION:  Humanized Antibodies Reactive with
;  TITLE OF INVENTION:  GPIIB/IIIA
;  NUMBER OF SEQUENCES:  23
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  William M. Smith
;    STREET:  One Market Plaza, Steuart Tower, Suite 2000
;    CITY:  San Francisco
;    STATE:  California
;    COUNTRY:  USA
;    ZIP:  94105
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Floppy disk
;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  Patentin Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/08/458,516
;    FILING DATE:
;    CLASSIFICATION:  424
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/059,159
;    FILING DATE:  03-MAY-1993
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  Smith, William M.
;    REGISTRATION NUMBER:  30,223
;    REFERENCE/DOCKET NUMBER:  1,823-37-3
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  415-326-2400
;    TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  N-terminal fragment
US-08-458-516-11

Query Match             90.3%;  Score 554.5;  DB 1;  Length 119;
Best Local Similarity   91.6%;  Pred. No. 5.4e-45;
Matches 109;  Conservative  3;  Mismatches  4;  Indels  3;  Gaps  2;

Qy         1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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Qy    1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 60
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Db   61 NEKFKGKATLTADKSSTAYMQlSSLTSDDSAVYFCA-RDG--PWFAYWGQGLEWIGVIYPGSGGTNY 60
Qy   61 NEKFKGKATLTVDKSSTAYMQlSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 119
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RESULT 2
US-08-458-516-7
; Sequence 7, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-7

Query Match   90.3%; Score 554.5; DB 1; Length 138;
Best Local Similarity   91.6%; Pred. No. 6.4e-45;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

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Qy    1 QVQLQQSGAELVRPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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Db   20 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 79
Qy   61 NEKFKGKATLTADKSSTAYMQlSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
          |||||||||||:||||||||||||||||||||||| ||| |||||||||:|||||||
Db   80 NEKFKGKATLTVDKSSTAYMQlSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 138
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RESULT 3
US-08-767-128-10
; Sequence 10, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH

; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 611079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-10

Query Match   89.0%; Score 546.5; DB 3; Length 119;
Best Local Similarity   89.9%; Pred. No. 3e-44;
Matches 107; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

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Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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Db    1 EVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
Qy   61 NEKFKGKATLTADKSSTAYMQlSSLTSDDSAVYFCARDGP--WFAYWGQGTLVTVSA 116
          ||||||||||||||||||||||||||||||||||| ::     :  : ::  ::::
Db   61 NEKFKGKATLTADKSSTAYMQlSSLTSDDSAVYFCARSGYGHWYFDVWGAGTTVTVSS 119
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RESULT 4
US-08-589-939-1
; Sequence 1, Application US/08589939
; Patent No. 6015662
; GENERAL INFORMATION:
; APPLICANT: Hackett, Jr., John R.

```
;  APPLICANT: Hoff, Jane A.
;  APPLICANT: Ostrow, David H.
;  APPLICANT: Golden, Alan M.
;  TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND
;  TITLE OF INVENTION: CONTROLS
;  NUMBER OF SEQUENCES: 70
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Abbott Laboratories
;  STREET: 100 Abbott Park Road
;  CITY: Abbott Park
;  STATE: IL
;  COUNTRY: US
;  ZIP: 60064-3500
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/589,939
;  FILING DATE:
;  CLASSIFICATION: 424
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Becker, Cheryl L.
;  REGISTRATION NUMBER: 35,441
;  REFERENCE/DOCKET NUMBER: 5865.US.01
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 847-935-1729
;  TELEFAX: 847-938-2623
;INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 138 amino acids
;  TYPE: amino acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-589-939-1

Query Match             83.1%;  Score 510.5;  DB 3;  Length 138;
Best Local Similarity   84.9%;  Pred. No. 8.5e-41;
Matches  101;  Conservative    5;  Mismatches   10;  Indels    3;  Gaps    1;

Qy          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
              ||:|||||||||||||||||||||||||||||||||| |||||||||||||:| |
Db         20 QVHLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWTQRPGQGLEWIGVINPGSDFTYY 79

Qy         61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR---DGPWFAYWGQGTLVTVSA 116
              ||||||||||||||||||||||:|||||||||||||||   : ::||||||||:
Db         80 NEKFKGKATLTADKSSSTAYMQLTSLTSDDSAVYFCARTIVTTDYFDYWGQGTPLTVSS 138


RESULT 5
US-08-458-516-10
;  Sequence 10, Application US/08458516
;  Patent No. 5777085
;  GENERAL INFORMATION:
;  APPLICANT: Co, Man Sung
;  APPLICANT: Tso, J. Yun
;  TITLE OF INVENTION: Humanized Antibodies Reactive with
;  TITLE OF INVENTION: GPIIB/IIIA
;  NUMBER OF SEQUENCES: 23
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: William M. Smith
;  STREET: One Market Plaza, Steuart Tower, Suite 2000
;  CITY: San Francisco
;  STATE: California
;  COUNTRY: USA
;  ZIP: 94105
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC Compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
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;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/458,516
;  FILING DATE:
;  CLASSIFICATION: 424
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/059,159
;  FILING DATE: 03-MAY-1993
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Smith, William M.
;  REGISTRATION NUMBER: 30,223
;  REFERENCE/DOCKET NUMBER: 11823-37-3
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 415-326-2422
;  TELEFAX: 415-326-2400
;INFORMATION FOR SEQ ID NO: 10:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 119 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
;  FRAGMENT TYPE: N-terminal fragment
US-08-458-516-10

Query Match             82.0%;  Score 503.5;  DB 1;  Length 119;
Best Local Similarity   80.7%;  Pred. No. 3.3e-40;
Matches   96;  Conservative   12;  Mismatches    8;  Indels    3;  Gaps    2;

Qy          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
              ||||:|||||:::||:|||||||||||||||||||||:| :|||||||||||:| |||||
Db          1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60

Qy         61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
              ||||||:.||| |::::|||||:|||::|:::|||||| :||   ||||||||||||||:
Db         61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119


RESULT 6
US-08-458-516-22
;  Sequence 22, Application US/08458516
;  Patent No. 5777085
;  GENERAL INFORMATION:
;  APPLICANT: Co, Man Sung
;  APPLICANT: Tso, J. Yun
;  TITLE OF INVENTION: Humanized Antibodies Reactive with
;  TITLE OF INVENTION: GPIIB/IIIA
;  NUMBER OF SEQUENCES: 23
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: William M. Smith
;  STREET: One Market Plaza, Steuart Tower, Suite 2000
;  CITY: San Francisco
;  STATE: California
;  COUNTRY: USA
;  ZIP: 94105
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/458,516
;  FILING DATE:
;  CLASSIFICATION: 424
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/059,159
;  FILING DATE: 03-MAY-1993
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Smith, William M.
;  REGISTRATION NUMBER: 30,223
;  REFERENCE/DOCKET NUMBER: 11823-37-3
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 415-326-2422
;  TELEFAX: 415-326-2400
;INFORMATION FOR SEQ ID NO: 22:
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;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 222 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-458-516-22

Query Match    82.0%;  Score 503.5;  DB 1;  Length 222;
Best Local Similarity  80.7%;  Pred. No. 6.4e-40;
Matches  96;  Conservative  12;  Mismatches  8;  Indels  3;  Gaps  2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
         ||||  ||||: :||:||||||||||||||||||| |||||||||||||| ||||||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60

Qy  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
         ||||| |||: |:::||:||:||||| |:|||||||| ||:     |||||||||||||:
Db  61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
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RESULT 7
US-08-458-516-23

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; Sequence 23, Application US/0845816
; Patent No. 5777085
; GENERAL INFORMATION:
;   APPLICANT: Co, Man Sung
;   APPLICANT: Tso, J. Yun
;   TITLE OF INVENTION: Humanized Antibodies Reactive with
;   TITLE OF INVENTION: GPIIB/IIIA
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: William M. Smith
;     STREET: One Market Plaza, Steuart Tower, Suite 2000
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/458,516
;     FILING DATE:
;     CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/059,159
;     FILING DATE: 03-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William M.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 11823-37-3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-326-2400
;     TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 23:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 235 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-458-516-23

Query Match    82.0%;  Score 503.5;  DB 1;  Length 235;
Best Local Similarity  80.7%;  Pred. No. 6.8e-40;
Matches  96;  Conservative  12;  Mismatches  8;  Indels  3;  Gaps  2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
         ||||  ||||: :||:||||||||||||||||||| |||||||||||||| ||||||||
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Qy  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
         ||||| |||: |:::||:||:||||| |:|||||||| ||:     |||||||||||||:
Db  61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
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RESULT 8
US-08-458-516-13

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; Sequence 13, Application US/0845816
; Patent No. 5777085
; GENERAL INFORMATION:
;   APPLICANT: Co, Man Sung
;   APPLICANT: Tso, J. Yun
;   TITLE OF INVENTION: Humanized Antibodies Reactive with
;   TITLE OF INVENTION: GPIIB/IIIA
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: William M. Smith
;     STREET: One Market Plaza, Steuart Tower, Suite 2000
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/458,516
;     FILING DATE:
;     CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/059,159
;     FILING DATE: 03-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Smith, William M.
;     REGISTRATION NUMBER: 30,223
;     REFERENCE/DOCKET NUMBER: 11823-37-3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-326-2400
;     TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 449 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-458-516-13

Query Match    82.0%;  Score 503.5;  DB 1;  Length 449;
Best Local Similarity  80.7%;  Pred. No. 1.4e-39;
Matches  96;  Conservative  12;  Mismatches  8;  Indels  3;  Gaps  2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
         ||||  ||||: :||:||||||||||||||||||| |||||||||||||| ||||||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60

Qy  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
         ||||| |||: |:::||:||:||||| |:|||||||| ||:     |||||||||||||:
Db  61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119
```

RESULT 9
US-09-157-370-2

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; Sequence 2, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
;   APPLICANT: STEIPE, Boris
;   APPLICANT: STEINBACHER, Stefan
;   TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
;   FILE REFERENCE: P8341-8072
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;   CURRENT APPLICATION NUMBER: US/09/157,370A
;   CURRENT FILING DATE: 1998-09-21
;   EARLIER APPLICATION NUMBER: 08/755,179
;   EARLIER FILING DATE: 1997-01-14
;   EARLIER APPLICATION NUMBER: PCT/EP95/02626
;   EARLIER FILING DATE: 1995-07-06
;   EARLIER APPLICATION NUMBER: DE/P44 25 115.7
;   EARLIER FILING DATE: 1994-07-15
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-157-370-2

Query Match   81.0%;   Score 497.5;   DB 3;   Length 117;
Best Local Similarity   80.3%;   Pred. No. 1.2e-39;
Matches 94;   Conservative 11;   Mismatches 11;   Indels 1;   Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          :|||||||:|| ||||:||||||||| ||:||||||||||||| ||||||||||
Db   1 EVQLQQSGGELVKPGASVKLSCKASGYTFTSYYMHWVKQRPGKGLEWIGRINPGSGGTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG-PWFAYWGQGTLVTVSA 116
          |||||||||:||||||| :|||||||||:|||||| ||: |||||||||||||
Db   61 NEKFKGKATLTRDKSSSTAYLQLSSLTSEDSAVYYCARGGYYFDYWGQGTTVTVSS 117

RESULT 10
US-08-767-128-20
; Sequence 20, Application US/08767128
; Patent No.6111079
; GENERAL INFORMATION:
;   APPLICANT: WYLIE, DWANE E.
;   APPLICANT: LOPEZ, OSVALDO
;   APPLICANT: MURRAY, PETER JOSEPH
;   APPLICANT: GOEBEL, PETER
;   TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
;   TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
;   NUMBER OF SEQUENCES: 46
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
;   STREET: 3100 No. 6111079west Center, 90 South Seventh St
;   CITY: Minneapolis
;   STATE: MN
;   COUNTRY: USA
;   ZIP: 55402
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/767,128
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE: 04-DEC-1996
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US96/09258
;   FILING DATE: 05-JUN-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/541,373
;   FILING DATE: 10-OCT-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,798
;   FILING DATE: 05-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Carter, Charles G.
;   REGISTRATION NUMBER: 35,093

;   REFERENCE/DOCKET NUMBER: 8848.49USF1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 612/371-5278
;   TELEFAX: 612/332-9081
;   TELEX:
; INFORMATION FOR SEQ ID NO: 20:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 119 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: internal
;   ORIGINAL SOURCE:
US-08-767-128-20

Query Match   79.9%;   Score 490.5;   DB 3;   Length 119;
Best Local Similarity   78.2%;   Pred. No. 5.4e-39;
Matches 93;   Conservative 10;   Mismatches 13;   Indels 3;   Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          |||||||:|||:|||||:| ::|||||| ||:||||||||||||| ||:||||||||||
Db   1 QVQLQQSGVELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR--DGPWFAYWGQGTLVTVSA 116
          |||||||||||||:|||||::| |||||||||:||:||| |||:||||||:|||||
Db   61 NEKFKGKATFTADTSSNTAYMQVSSLTSEDSAVYYCARIIYGHLWFAYWGQGTLVTVSA 119

RESULT 11
US-08-881-037-65
; Sequence 65, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
;   APPLICANT: Glick, Gary D.
;   APPLICANT: Swanson, Patrick C.
;   TITLE OF INVENTION: DNA BINDING ANTIBODIES
;   NUMBER OF SEQUENCES: 113
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Morrison & Foerster
;   STREET: 755 Page Mill Road
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/881,037
;   FILING DATE: 23-JUN-1997
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/443,540
;   FILING DATE: 18-MAY-1995
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Konski, Antoinette F.
;   REGISTRATION NUMBER: 34,202
;   REFERENCE/DOCKET NUMBER: 20344211071O
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 813-5600
;   TELEFAX: (650) 494-0792
;   TELEX:
; INFORMATION FOR SEQ ID NO: 65:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 121 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single

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;   TOPOLOGY: linear
US-08-881-037-65

Query Match          79.1%;  Score 485.5;  DB 3;  Length 121;
Best Local Similarity  80.0%;  Pred. No. 1.6e-38;
Matches   96;  Conservative    4;  Mismatches   15;  Indels    5;  Gaps    1;

Qy   1  QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY  60
        |||  |:|||||||||||||||||||||||||||: |: |||||:||||:|||:|||||||
Db   1  QVQLLESGAELARPGASVKLSCKASGYTFTSYGISWVKQRTGQGLEWIGEIYPRSGNTYY  60

Qy  61  NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG-----PWFAYWGQGTLVTVS  115
        |||||||||||||||||   ||||||||||||||||||||      |||||||||||||||
Db  61  NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARQSYSYSWFAYWGQGTLVTVS   120


RESULT 12
US-08-737-560A-10
; Sequence 10, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
;   APPLICANT: KANG, Chang-Yuil
;   APPLICANT: KIM, Joong-Gon
;   TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
;   TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
;   NUMBER OF SEQUENCES: 13
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: KANG, Chang-Yuil
;   STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
;   CITY: Seoul
;   STATE: Seoul
;   COUNTRY: Republic of Korea
;   ZIP: 151-057
;   ADDRESSEE: KIM, Joong-Gon
;   STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
;   CITY: Seoul
;   STATE: Seoul
;   COUNTRY: Republic of Korea
;   ZIP: 135-110
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
;   COMPUTER: IBM PC/AT
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: Word Perfect 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/737,560A
;   FILING DATE: 13-NOV-1996
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: KR 95-8176
;   FILING DATE: 08-APR-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME:
;   REGISTRATION NUMBER:
;   REFERENCE/DOCKET NUMBER:
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:
;   TELEFAX:
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 119 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FEATURE:
;   OTHER INFORMATION: 4B4-1-1 heavy chain variable region
US-08-737-560A-10

Query Match          78.6%;  Score 482.5;  DB 2;  Length 119;
Best Local Similarity  79.0%;  Pred. No. 3e-38;
Matches   94;  Conservative    8;  Mismatches   14;  Indels    3;  Gaps    1;
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Qy   1  QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY  60
        |||  |:||||||:|||||||||||||||||||:|:: ||||||||||||:|||||||||
Db   1  QVQLQQPGAELVKPGASVKLSCKASGYTFSSYWMWVKQRPGQVLEWIGEINPGNGHTNY   60

Qy  61  NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA  116
        |||||:||||||:||||||||||||||||:||||||||||    ||||||||||||||||
Db  61  NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARSFTTARGFAYWGQGTLVTVSA  119


RESULT 13
US-07-916-098A-10
; Sequence 10, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
;   APPLICANT: BURKLY, LINDA C.
;   APPLICANT: CHISHOLM, PATRICIA L.
;   APPLICANT: THOMAS, DAVID W.
;   APPLICANT: ROSA, MARGARET D.
;   APPLICANT: ROSA, JOSEPH J.
;   TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;   TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;   NUMBER OF SEQUENCES: 61
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
;   STREET: 10 SOUTH WACKER DRIVE
;   CITY: CHICAGO
;   STATE: ILLINOIS
;   COUNTRY: U.S.A.
;   ZIP: 60606
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/916,098A
;   FILING DATE: July 24, 1992
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US91/08843
;   FILING DATE: No. 5871732ember 27, 1991
;   CLASSIFICATION: 424
;   APPLICATION NUMBER: 07/618,542
;   FILING DATE: No. 5871732ember 27, 1990
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: JOHN J. MC DONNELL
;   REGISTRATION NUMBER: 26,949
;   REFERENCE/DOCKET NUMBER: 92,310-G
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (312) 715-1000
;   TELEFAX: (312) 715-1234
;   TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 122 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-07-916-098A-10

Query Match          78.5%;  Score 482;  DB 2;  Length 122;
Best Local Similarity  72.1%;  Pred. No. 3.5e-38;
Matches   88;  Conservative   19;  Mismatches   9;  Indel.s    6;  Gaps    1;

Qy   1  QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY  60
        ::|||| ||:|||:|||||||||| :|||:|:||||||||||||:|||||:|||||:||||
Db   1  EVKLQESGPEILVKPGASVKMSCKASGYTTSYVIHWVKQKPGQGLDWIGYINPYNDGTDY  60

Qy  61  NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD------GPWFAYWGQGTLVTV  114
        ||||||||||| |||   |:||:|||::|||||:||||:        |||||||||:||||
Db  61  DEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCAREKDNYATGAWFAYWGQGTTVTV  120
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Qy   115 SA 116
            |:|
Db   121 SS 122

RESULT 14
US-09-438-954-39
; Sequence 39, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
;   APPLICANT: HONG, Hyo Jeong
;   APPLICANT: PARK, Sung Sup
;   APPLICANT: KANG, Young Jun
;   APPLICANT: KANG, Chang-Yuil
;   APPLICANT: YOON, Sung Kwan
;   TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
;   TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
;   FILE REFERENCE: 1303-124P
;   CURRENT APPLICATION NUMBER: US/09/438,954
;   CURRENT FILING DATE: 1999-11-12
;   NUMBER OF SEQ ID NOS: 49
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Variable
;   OTHER INFORMATION: region of heavy chain of mouse monoclonal antibody
;   OTHER INFORMATION: 4B4-1-1
US-09-438-954-39

Query Match   78.4%; Score 481.5; DB 4; Length 119;
Best Local Similarity   79.0%; Pred. No. 3.8e-38;
Matches   94; Conservative   8; Mismatches   14; Indels   3; Gaps   1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
            ||||||||||||| |||:|| |||||||||||:||:: ||||||||||||: ||||| ||
Db   1 QVQLQQPGAELVKPGASVKLSCKASGYTFSSYWMHWVKQRPGQVLEWIGEINPGNGHTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA 116
            ||||||||||| ||||:|||||||||:||:|||||||| |||||||||||||||||
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RESULT 15
US-08-392-419-2
; Sequence 2, Application US/08392419
; Patent No. 5624659
; GENERAL INFORMATION:
;   APPLICANT: Bigner, Darell D.
;   APPLICANT: Zalutsky, Michael R.
;   TITLE OF INVENTION: METHOD OF TREATMENT
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Kenneth D. Sibley
;   STREET: P.O. Drawer 34009
;   CITY: Charlotte
;   STATE: No. 562465 9th Carolina
;   COUNTRY: USA
;   ZIP: 28234
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/392,419
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/033,827
;   FILING DATE: 19-MAR-1993

;   ATTORNEY/AGENT INFORMATION:
;   NAME: Sibley, Kenneth D.
;   REGISTRATION NUMBER: 31,665
;   REFERENCE/DOCKET NUMBER: 5405-90
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 919-420-2200
;   TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 137 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-392-419-2

Query Match   78.2%; Score 480; DB 1; Length 137;
Best Local Similarity   77.1%; Pred. No. 6.1e-38;
Matches   91; Conservative   12; Mismatches   13; Indels   2; Gaps   1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
            :||||||||||| ||| |||||||||:||::: ||::: |||| ||||||: |||||
Db   20 EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVVHWVKQNPGQGLEWIGYINPFNDGTKY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSLTSDDSAVYFCARD--GPWFAYWGQGTLVTVSA 116
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Db   80 NENFKGKATLTSDRSSSTAYMELSSLTSEESAVYFCARDMGREGFAYWGQGTLVTVSA 137

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Job time : 16.0852 secs

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OM protein - protein search, using sw model

            GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:      August 16, 2004, 11:10:36 ; Search time 42.1345 Seconds
                                          (without alignments)
                                          864.269 Million cell updates/sec

Title:       US-09-889-300A-1
Perfect score: 614
Sequence:    1 QVQLQQSGAELVRPGTSVKV.........ARDGPWFAYWGQGTLVTVSA 116

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Searched:    1292805 seqs, 31392144 residues

Total number of hits satisfying chosen parameters:     1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA:*
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        7:  /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
        8:  /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
        9:  /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
       10:  /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
       11:  /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
       12:  /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
       13:  /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
       14:  /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
       15:  /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
       16:  /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
       17:  /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
       18:  /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	554.5	90.3	119	12	US-10-411-037-54	Sequence 54, Appl
2	554.5	90.3	119	12	US-10-411-026-54	Sequence 54, Appl
3	554.5	90.3	119	16	US-10-410-962-54	Sequence 54, Appl
4	554.5	90.3	119	16	US-10-411-049-54	Sequence 54, Appl
5	554.5	90.3	119	16	US-10-410-930-54	Sequence 54, Appl
6	554.5	90.3	119	16	US-10-410-997-54	Sequence 54, Appl
7	554.5	90.3	119	16	US-10-411-012-54	Sequence 54, Appl
8	554.5	90.3	119	16	US-10-287-994-54	Sequence 54, Appl
9	554.5	90.3	119	16	US-10-410-913-54	Sequence 54, Appli
10	519	84.5	138	13	US-10-146-305-8	Sequence 8, Appli
11	503.5	82.0	119	12	US-10-411-037-53	Sequence 53, Appl
12	503.5	82.0	119	12	US-10-411-026-53	Sequence 53, Appl
13	503.5	82.0	119	16	US-10-410-962-53	Sequence 53, Appl
14	503.5	82.0	119	16	US-10-411-049-53	Sequence 53, Appl
15	503.5	82.0	119	16	US-10-410-930-53	Sequence 53, Appl
16	503.5	82.0	119	16	US-10-410-997-53	Sequence 53, Appl
17	503.5	82.0	119	16	US-10-411-012-53	Sequence 53, Appl
18	503.5	82.0	119	16	US-10-287-994-53	Sequence 53, Appl
19	503.5	82.0	119	16	US-10-410-913-53	Sequence 53, Appl
20	503.5	82.0	448	12	US-10-411-037-56	Sequence 56, Appl
21	503.5	82.0	448	12	US-10-411-026-56	Sequence 56, Appl
22	503.5	82.0	448	16	US-10-410-962-56	Sequence 56, Appl
23	503.5	82.0	448	16	US-10-411-049-56	Sequence 56, Appl
24	503.5	82.0	448	16	US-10-410-930-56	Sequence 56, Appl
25	503.5	82.0	448	16	US-10-410-997-56	Sequence 56, Appl
26	503.5	82.0	448	16	US-10-411-012-56	Sequence 56, Appl
27	503.5	82.0	448	16	US-10-287-994-56	Sequence 56, Appl
28	503.5	82.0	448	16	US-10-410-913-56	Sequence 56, Appl
29	490.5	79.9	113	16	US-10-307-276B-11	Sequence 11, Appl
30	489	79.6	139	13	US-10-006-773-13	Sequence 13, Appl
31	488	79.5	118	15	US-10-435-614-11	Sequence 11, Appl
32	488	79.5	260	15	US-10-435-614-20	Sequence 20, Appl
33	486	79.2	118	15	US-10-435-614-13	Sequence 13, Appl
34	486	79.2	177	15	US-10-435-614-21	Sequence 21, Appl
35	485.5	79.1	113	16	US-10-307-276B-5	Sequence 5, Appli
36	485.5	79.1	113	16	US-10-307-276B-7	Sequence 7, Appli
37	485.5	79.1	117	15	US-10-447-257-2	Sequence 2, Appli
38	485.5	79.1	143	14	US-10-010-729-66	Sequence 66, Appli
39	485	79.0	118	16	US-10-467-546-2	Sequence 2, Appli
40	485	79.0	448	16	US-10-467-546-4	Sequence 4, Appli
41	483.5	78.7	119	12	US-10-153-024-2	Sequence 2, Appli
42	483	78.7	195	14	US-10-360-053-6	Sequence 6, Appli
43	483	78.7	195	14	US-10-360-053-8	Sequence 8, Appli
44	482.5	78.6	113	16	US-10-307-276B-3	Sequence 3, Appli
45	482.5	78.6	119	12	US-10-460-595-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-411-037-54
; Sequence 54, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; TITLE OF INVENTION: GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-037-54

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Query Match              90.3%;    Score 554.5;  DB 12;  Length 119;
Best Local Similarity    91.6%;    Pred. No. 1.8e-45;
Matches   109;  Conservative  3;  Mismatches  4;  Indels  3;  Gaps  2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
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Db   1 QVQLQQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 60

Qy  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
         |||||||||| |||||| ||||||||||||||||||| ||| |||     |||| |||||||
Db  61 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 119
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RESULT 2
US-10-411-026-54
; Sequence 54, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-026-54

```
Query Match              90.3%;    Score 554.5;  DB 12;  Length 119;
Best Local Similarity    91.6%;    Pred. No. 1.8e-45;
Matches   109;  Conservative  3;  Mismatches  4;  Indels  3;  Gaps  2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
         ||||||| |||||| |||||| ||||||||||||||||||||||||||||||||| ||||||||
Db   1 QVQLQQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 60

Qy  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
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Db  61 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 119
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RESULT 3
US-10-410-962-54
; Sequence 54, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-962-54

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Query Match              90.3%;    Score 554.5;  DB 16;  Length 119;
Best Local Similarity    91.6%;    Pred. No. 1.8e-45;
Matches   109;  Conservative  3;  Mismatches  4;  Indels  3;  Gaps  2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
         ||||||| |||||| |||||| ||||||||||||||||||||||||||||||||| ||||||||
Db   1 QVQLQQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY 60

Qy  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
         |||||||||| |||||| |||||||||||||||||||| ||| |||     |||| |||||||
Db  61 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA 119
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RESULT 4
US-10-411-049-54
; Sequence 54, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERO
; TITLE OF INVENTION: ALPHA
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-049-54

Query Match   90.3%;   Score 554.5;   DB 16;   Length 119;
Best Local Similarity   91.6%;   Pred. No. 1.8e-45;
Matches 109; Conservative   3;   Mismatches   4;   Indels   3;   Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY   60
          ||||||||||||| ||||||::||||||||||||||||||||||||||||| |||||||
Db   1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY   60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA   116
          |||||||||| || |||||||||||||||||||||||| ||| |||||||||:||||||
Db   61 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA   119

RESULT 5
US-10-410-930-54
; Sequence 54, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; TITLE OF INVENTION: BETA
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-930-54

Query Match   90.3%;   Score 554.5;   DB 16;   Length 119;
Best Local Similarity   91.6%;   Pred. No. 1.8e-45;
Matches 109; Conservative   3;   Mismatches   4;   Indels   3;   Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY   60
          ||||||||||||| ||||||::||||||||||||||||||||||||||||| |||||||
Db   1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY   60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA   116
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Db   61 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA   119

RESULT 6
US-10-410-997-54
; Sequence 54, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
; TITLE OF INVENTION: FSH
; FILE REFERENCE: 040853-01-5059
; CURRENT APPLICATION NUMBER: US/10/410,997
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-997-54

Query Match   90.3%;   Score 554.5;   DB 16;   Length 119;
Best Local Similarity   91.6%;   Pred. No. 1.8e-45;
Matches 109; Conservative   3;   Mismatches   4;   Indels   3;   Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY   60
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Db   1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY   60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA   116
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Db   61 NEKFKGKATLTVDKSSTTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA   119

RESULT 7
US-10-411-012-54
; Sequence 54, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10

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Matches  109;    Conservative   3;    Mismatches   4;    Indels   3;    Gaps   2;

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Db    1  QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY   60

Qy   61  NEKFKGKATLTADKSSSTAYMQLSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA   116
         |||||||||||  |||||||||||||  ||||||||||   ||   |:|| |||||||||
Db   61  NEKFKGKATLTVDKSSTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA    119
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RESULT 9
US-10-410-913-54
; Sequence 54, Application US/10410913
; Publication No. US20040142855A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Bowe, Caryn
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5081
; CURRENT APPLICATION NUMBER: US/10/410,913
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-913-54

Query Match   90.3%;   Score 554.5;   DB 16;   Length 119;
Best Local Similarity   91.6%;   Pred. No. 1.8e-45;
Matches 109;   Conservative   3;   Mismatches   4;   Indels   3;   Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY   60
         |||||||||||| |||||| |||||||||||||||||||||||||||||||| |||||||
Db   1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY   60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA   116
         ||||||||||| ||||||||||||| |||||||||| || |:|| |||||||||
Db   61 NEKFKGKATLTVDKSSTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA   119
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RESULT 10
US-10-146-305-8
; Sequence 8, Application US/10146305
; Publication No. US20020173035A1
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: OV17440
; CURRENT APPLICATION NUMBER: US/10/146,305

; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-012-54

Query Match   90.3%;   Score 554.5;   DB 16;   Length 119;
Best Local Similarity   91.6%;   Pred. No. 1.8e-45;
Matches 109;   Conservative   3;   Mismatches   4;   Indels   3;   Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY   60
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Db   1 QVQLQQSGAELVGPGTSVRVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVIYPGSGGTNY   60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA   116
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Db   61 NEKFKGKATLTVDKSSTAYMQLSSLTSDDSAVYFCARRDGNYGWFAYWGRGTLVTVSA   119

RESULT 8
US-10-287-994-54
; Sequence 54, Application US/10287994
; Publication No. US20040137557A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-00
; CURRENT APPLICATION NUMBER: US/10/287,994
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-287-994-54

Query Match   90.3%;   Score 554.5;   DB 16;   Length 119;
Best Local Similarity   91.6%;   Pred. No. 1.8e-45;
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; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-8

Query Match　　　84.5%;　Score 519;　DB 13;　Length 138;
Best Local Similarity　83.6%;　Pred. No. 5.3e-42;
Matches 102;　Conservative　5;　Mismatches　9;　Indels　6;　Gaps　1;

Qy　　　1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　1 QVQLQQSGTEWVRPGTSVKVSCKASGYPF'NHLIEWVKQRPGQGPEWIGVINPGSGGTNY 60

Qy　　　61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-----RDGPWFAYWGQGTLVTV 114
　　　　　|||||||||||||||||||||||||||||||:|　　||||　|||
Db　　　61 NEKFKGKATLTADKSSSTAYMQLNSLTSDDSAVYFCAIMTTFLGEGYAMDYWGQGTSVTV 120

Qy　　　115 SA 116
　　　　　|:|
Db　　　121 SS 122

RESULT 11
US-10-411-037-53
; Sequence 53, Application US/10411037
; Publication No.US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; TITLE OF INVENTION: GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE:　2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-037-53

Query Match　　　82.0%;　Score 503.5;　DB 12;　Length 119;
Best Local Similarity　80.7%;　Pred. No. 1.4e-40;
Matches　96;　Conservative　12;　Mismatches　8;　Indels　3;　Gaps　2;

Qy　　　1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
　　　　　|||||||||:||:|||||||||||||||||||||||||||||||||||||||||||||||

---

Db　　　1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIPGSGGTNY 60

Qy　　　61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
　　　　　|||||||:||||:|:||||||||||||||||||||:|||||　||：|||||||||||：
Db　　　61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVFCARRDGNYGWFAYWGQGTLVTVSS 119

RESULT 12
US-10-411-026-53
; Sequence 53, Application US/10411026
; Publication No.US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE:　2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-53

Query Match　　　82.0%;　Score 503.5;　DB 12;　Length 119;
Best Local Similarity　80.7%;　Pred. No. 1.4e-40;
Matches　96;　Conservative　12;　Mismatches　8;　Indels　3;　Gaps　2;

Qy　　　1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
　　　　　|||||||:||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIPGSGGTNY 60

Qy　　　61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
　　　　　|||||||:||||:|:||||||||||||||||||||:|||||　||:|||||||||||:
Db　　　61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVFCARRDGNYGWFAYWGQGTLVTVSS 119

RESULT 13
US-10-410-962-53
; Sequence 53, Application US/10410962
; Publication No.US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
; FILE REFERENCE: 040853-01-5054

RESULT 14
US-10-411-049-53
; Sequence 53, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; TITLE OF INVENTION: ALPHA
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-049-53

Query Match      82.0%;  Score 503.5;  DB 16;  Length 119;
Best Local Similarity  80.7%;  Pred. No. 1.4e-40;
Matches  96;  Conservative  12;  Mismatches  8;  Indels  3;  Gaps  2;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||| |||||||| :: :|:||||||||||||||||||||||| ||||||||| ||||||
Db    1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
          ||||||| ||| |:| ||::||||||||||||||||| : |:|||||||||||||:
Db   61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119

RESULT 15
US-10-410-930-53
; Sequence 53, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; TITLE OF INVENTION: BETA
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-930-53

Query Match      82.0%;  Score 503.5;  DB 16;  Length 119;
Best Local Similarity  80.7%;  Pred. No. 1.4e-40;
Matches  96;  Conservative  12;  Mismatches  8;  Indels  3;  Gaps  2;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||| |||||||| :: :|:||||||||||||||||||||||| ||||||||| ||||||
Db    1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA-RDG--PWFAYWGQGTLVTVSA 116
          ||||||| ||| |:| ||::||||||||||||||||| : |:|||||||||||||:
Db   61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDTAVYFCARRDGNYGWFAYWGQGTLVTVSS 119

Search completed: August 16, 2004, 11:21:19
Job time : 43.1345 secs

us-09-889-300a-1.rpr

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                    GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   August 16, 2004, 11:08:06 ; Search time 12.4843 Seconds
                                      (without alignments)
                                      893.780 Million cell updates/sec

Title:        US-09-889-300A-1
Perfect score: 614
Sequence:   1 QVQLQQSGAELVRPGTSVKV........ARDGPWFAYWGQGTLVTVSA 116

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:     283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:    283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    PIR_78:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	535.5	87.2	123	2	B30560	Ig heavy chain V r
2	526	85.7	123	2	S60067	Ig heavy chain V r
3	491.5	80.0	119	2	S20640	Ig heavy chain V r
4	491	80.0	135	2	A30577	Ig heavy chain pre
5	487.5	79.4	117	2	JC2269	PL7-6 antibody hea
6	487.5	79.4	119	2	C30562	Ig heavy chain V r
7	487	79.3	474	2	G2MS11	Ig gamma-2b chain
8	485	79.0	137	2	F29380	Ig heavy chain pre
9	484	78.8	118	2	C30560	Ig heavy chain V r
10	483.5	78.7	118	2	S38565	Ig heavy chain V r
11	483.5	78.7	138	2	S21810	Ig heavy chain V r
12	482.5	78.6	246	2	S38950	Ig gamma chain - m
13	482.5	78.6	446	2	S40295	Ig gamma-2a chain
14	481.5	78.4	119	2	E30562	Ig heavy chain V r
15	481	78.3	141	2	JL0076	Ig heavy chain V r
16	478.5	77.9	119	2	D30562	Ig heavy chain pre
17	478	77.9	137	2	E29380	Ig heavy chain pre
18	477.5	77.8	131	2	A27472	Ig heavy chain pre
19	476	77.5	140	2	S09216	Ig heavy chain pre
20	475.5	77.4	138	1	HVMST7	Ig heavy chain pre
21	475	77.4	115	2	A54378	Ig heavy chain V r
22	473.5	77.1	140	2	PH1482	Ig heavy chain V r
23	472.5	77.0	118	2	PL0231	Ig heavy chain V r
24	470	76.5	119	2	A24672	Ig heavy chain pre
25	469.5	76.5	117	2	S19966	Ig heavy chain V r
26	469.5	76.5	140	1	HVMSG7	Ig heavy chain pre
27	468	76.2	116	2	S09962	Ig heavy chain V-D
28	468	76.2	116	2	S53751	antibody Fab Jel 1
29	467.5	76.1	123	2	E48677	Ig heavy chain V-D
30	466	75.9	112	2	A30502	Ig heavy chain V r
31	466	75.9	117	2	S25176	Ig heavy chain V r
32	466	75.9	139	1	MHMS18	Ig heavy chain pre
33	466	75.9	141	2	A39276	Ig heavy chain pre
34	466	75.9	287	4	PC4402	pelB leader/Ig hea
35	465.5	75.8	112	2	PL0232	Ig heavy chain V r
36	465.5	75.8	121	2	S19969	Ig heavy chain V r
37	465	75.7	118	2	S38717	Ig heavy chain V r
38	465	75.7	120	2	B22769	Ig heavy chain pre
39	464	75.6	131	2	S66537	Ig heavy chain V r
40	463.5	75.5	123	2	F48677	Ig heavy chain V-D
41	463.5	75.5	138	2	B32513	Ig heavy chain pre
42	462.5	75.3	115	2	A56700	Ig heavy chain (an
43	462.5	75.3	116	2	S55542	Ig heavy chain V r
44	460	74.9	118	2	S37201	Ig heavy chain V r
45	460	74.9	120	2	G28195	Ig heavy chain V r

ALIGNMENTS

RESULT 1
B30560
Ig heavy chain V region (28.4.10A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jul-1999
C;Accession: B30560
R;Matsuda, T.; Kabat, E.A.
J; Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monocl
A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: B30560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <MAT>
A;Cross-references: GB:M24269; NID:g195619; PIDN:AAA38373.1; PID:g195620
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

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Query Match       87.2%;  Score 535.5;  DB 2;  Length 123;
Best Local Similarity   87.8%;  Pred. No. 1.5e-41;
Matches  108;  Conservative  1;  Mismatches  7;  Indels  ;  Gaps  2;

Qy      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
            ||||||||||||||||||||||||||||||||||||||| ||  |||||||||||||||
Db      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRLGQDLEWIGVINPGSGGTNY 60

Qy     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR------DGPW-FAYWGQGTLVT 113
            ||||||||||||||||||||||||||||||||||||||      ||  ||||||||||
Db     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARSSPYDYGYWYFDVWGAGTTVT 120

Qy    114 VSA 116
          ||:
Db    121 VSS 123
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RESULT 2
S60067
Ig heavy chain V region (monoclonal antibody C3, gamma 2A) [validated] - mouse (fragment
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
C;Accession: S60067
R;Wien, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.; Hogl
Nat. Struct. Biol. 2, 232-243, 1995
A;Title: Structure of the complex between the fab fragment of a neutralizing antibody fo
A;Reference number: S60066; MUID:9529210; PMID:7539711
A;Accession: S60067
A;Molecule type: mRNA
A;Residues: 1-123 <WIE>
A;Cross-references: EMBL:X84698; NID:g773225
R;Wien, M.W.; Hogle, J.M.

submitted to the Brookhaven Protein Data Bank, January 1995
A;Reference number: A52979; PDB:1FPT
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-123
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-98/Domain: immunoglobulin homology <IMM>
F;i/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;22-96/Disulfide bonds: #status experimental

Query Match   85.7%;   Score 526; DB 2; Length 123;
Best Local Similarity   85.0%;   Pred. No. 1.1e-40; Indels 4; Gaps 1;
Matches   102; Conservative   5; Mismatches   9;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||::
Db   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIQWIKQRPGQGLEWIGVINPGGGTDY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA 116
          ||||||||||||||||||||||||||||||||||||||| :||||||||||||::
Db   61 NANFKGKATLTADKSSSIVYMQLSSLTSDDSAVYFCARDFYDYDVGFDYWGQGTTLTVSS 120

RESULT 3
S20640
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20640, S20644
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Accession: S20640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <LOS>
A;Cross-references: EMBL:X65002; NID:g52600; PIDN:CAA46135.1; PID:g52601; EMBL:X64999; N
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   80.0%;   Score 491.5; DB 2; Length 119;
Best Local Similarity   77.3%;   Pred. No. 1.4e-37;
Matches   92; Conservative 13; Mismatches 11; Indels 3; Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||||:||||||||||||||||||||| ||||||:|||||||||||||||||:::||
Db   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVIHWVKQKPGRGLEWIGVINPYNDGSKY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR--DGPWFAYWGQGTLVTVSA 116
          |||||||||||:||||||||||:|||:||:||||||||| :||:||||||||||||
Db   61 NEMFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARRATKGSWFAYWGQGTLVTVSA 119

RESULT 4
A30577
Ig heavy chain precursor V region (MRL10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C;Accession: A30577
R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof
J. Exp. Med. 161, 805-815, 1985
A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rela
A;Reference number: A30577; MUID:85159423; PMID:3920343
A;Accession: A30577
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <KOF>
A;Cross-references: GB:M37621
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match   80.0%;   Score 491; DB 2; Length 135;
Best Local Similarity   82.8%;   Pred. No. 1.7e-37;
Matches   96; Conservative   4; Mismatches 16; Indels 0; Gaps 0;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWNWVKQRPGQGLEWIGNIYPGSSSTNY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
          |||||||||||||||||||||||||||||||||||:|||| ||| ||||||||||
Db   80 NEKFKSKATLIVDTSSSTAYMQLSSLTSDDSSTAYMQLSSLTSDDSAVYYCARLVGGFAYWGQGTLVGGTLVTVSA 135

RESULT 5
JC2269
PL7-6 antibody heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: JC2269; PC2186
R;Kurome, T.; Katayama, M.; Murakami, K.; Hashino, K.; Kaminagi, K.; Yasumoto, M.; Ka
J. Biochem. 115, 608-614, 1994
A;Title: Expression of recombinant mouse/human chimeric antibody specific to human GM
A;Reference number: JC2269; MUID:9433410; PMID:7520038
A;Accession: JC2269
A;Molecule type: mRNA
A;Residues: 1-117 <KUR>
A;Accession: PC2186
A;Molecule type: protein
A;Residues: 2-27 <KU2>
A;Experimental source: hybridoma cell
C;Comment: This protein is specific to human P-selectin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;2-98/Region: V segment
F;15-98/Domain: immunoglobulin homology <IMM>
F;99-106/Region: D segment
F;107-117/Region: J segment

Query Match   79.4%;   Score 487.5; DB 2; Length 117;
Best Local Similarity   78.6%;   Pred. No. 3.1e-37;
Matches   92; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||||||||||||||||||||||||||:||:||||||||||||||||:|||||||||
Db   1 EVQLQQSGAELVKPGASVNMSCKASGYTFTSYWMHWVKQRPGQGLEWIGVINPGTAYTEH 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGP-WFAYWGQGTLVTVSA 116
          |||||||||||||||||||||||:|||:||||||||||::: ||||||||||||||
Db   61 NQKFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYCASGNPAWFAYWGQGTLVTVSA 117

RESULT 6
C30562
Ig heavy chain V region (27.7.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C;Accession: C30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison,
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: C30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   79.4%;   Score 487.5; DB 2; Length 119;
Best Local Similarity   79.0%;   Pred. No. 3.1e-37;
Matches   94; Conservative   9; Mismatches 13; Indels 3; Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60

```
Db        ||||||||||| ||| :|||||||||| ||| ||||||||||| :|||||||| ||:||||||||| |||||||| |||
        1 QVQLQQSGAELMKPGASVKISCKATGYTPSSYWIEWVKQRPGHGLEWIGEIIPGSGGTNY 60

Qy       61 NEKFKGKATILTADKSSSTAYMQLSLTSDDSAVYFCAR--DGPWFAYWGQGTLVTVSA 116
            ||||||||| ||| :||||||||||||:||:||| |||||
Db       61 NEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARHYYGSSSFAYWGQGTLVTVSA 119
```

RESULT 7
G2MS11
Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A;Reference number: S25057
A;Accession: S25057
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
A;Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 205, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11
A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Note: lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglc
A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
A;Molecule type: DNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A;Cross-references: GB:J00461
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu

F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   79.3%; Score 487; DB 1; Length 474;
Best Local Similarity 77.1%; Pred. No. 1.5e-36;
Matches 91; Conservative 11; Mismatches 14; Indels 2; Gaps 1;

```
Qy        1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
            :||||| |||||:||||:||||||||||||||||||||||:||||:|||||| || ||||
Db       20 EVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKPGQGLEWIGYINPNKDGTKF 79

Qy       61 NEKFKGKATILTADKSSSTAYMQLSSLTSDDSAVYFCAR--DGPWFAYWGQGTLVTVSA 116
            |||||||| |||||||: ||||:||:||||||||||| ||   ||||||||||||||||
Db       80 NEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCARDYDYDWFAYWGQGTLVTVSA 137
```

RESULT 8
F29380
Ig heavy chain precursor V region (A003 40/5G7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: F29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A;Reference number: A92612; MUID:88007582; PMID:3115981
A;Accession: F29380
A;Molecule type: mRNA
A;Residues: 1-137 <CHE>
A;Cross-references: GB:M17165; GB:J02815; NID:g195409; PIDN:AAA38294.1; PID:g195410
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IM1>

Query Match   79.0%; Score 485; DB 2; Length 137;
Best Local Similarity 79.7%; Pred. No. 6.1e-37;
Matches 94; Conservative 6; Mismatches 16; Indels 2; Gaps 1;

```
Qy        1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
            :||||| |||||||||:||||||||||||||||||||||:||||:|||| ||| ||||||
Db       20 QVQVQQPGAELVKPGTSVKLSCKASGYNFTTYWINWVKLRPGQGLEWIGDIYPSGSGTNY 79

Qy       61 NEKFKGKATILTADKSSSTAYMQLSSLTSDDSAVYFCARD--GPWFAYWGQGTLVTVSA 116
            |||||||| |||||||| |||||||||||||||||| |     ||||||||||||||||
Db       80 NEKFKSKATLIVDTSSTAYMQLSSLASEDSALYCARQVGETWFAYWGQGTLVTVSA 137
```

RESULT 9
C30560
Ig heavy chain V region (35.8.2H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999
C;Accession: C30560
R;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monocl
A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: C30560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <MAT>
A;Cross-references: GB:M24270; NID:g195615; PIDN:AAA38371.1; PID:g195616
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IM>

Query Match   78.8%; Score 484; DB 2; Length 118;
Best Local Similarity 78.0%; Pred. No. 6.4e-37;
Matches 92; Conservative 10; Mismatches 14; Indels 2; Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        ||||||||:|||:||||||| :||||||||| | || |||||||||||||||:| :| |
Db   1 QVHLQQSGAELVKPGASVKISCKASGYTFTSYWMWVKQRPGQGLEWIGEIDPSNSYTNN 60

Qy   61 NEKFKGKATLTADKSSTAYMQLSSLTSDDSAVYFCAR--DGPWFAYWGQGTLVTVSA 116
        |:|||:||||||||||:||||||||||:||||||:|| :||| |||||||||||||
Db   61 NQKFKNKATLTVDKSSNTAYMQLSSLTSEDSAVYYCARWGTGSWFAYWGQGTLVTVSA 118

RESULT 10
S38565
Ig heavy chain V region (ASWV1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38565
R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M
A;Reference number: S38559
A;Accession: S38565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <MON>
A;Cross-references: EMBL:X75100; NID:g414157; PIDN:CAA52991.1; PID:g414158
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   78.7%; Score 483.5; DB 2; Length 118;
Best Local Similarity 78.8%; Pred. No. 7.1e-37;
Matches 93; Conservative   9; Mismatches 13; Indels 3; Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        ||||||||:|||| ||||| |||||||||||| ||||||||||||||||:| :| |
Db   1 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKY 60

Qy   61 NEKFKGKATLTADKSSTAYMQLSSLTSDDSAVYFCARDGP---WFAYWGQGTLVTVS 115
        |||||||:|||:||||:|||||:||||:||||||||| || |||||||||||||
Db   61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCAREGAGSYYFDYWGQGTTLTVS 118

RESULT 11
S21810
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21810
R;Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
submitted to the EMBL Data Library, January 1991
A;Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy cha
A;Reference number: S21810
A;Accession: S21810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-138 <OST>
A;Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PID:g54164
A;Genetics:
A;Introns: 15/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match   78.7%; Score 483.5; DB 2; Length 138;
Best Local Similarity 79.8%; Pred. No. 8.4e-37;
Matches 95; Conservative   7; Mismatches 7; Indels 3; Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        ||||||||:||| |:|||| |||||||||||||||||||||||||||||:| :| |
Db   20 QVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRPGQGLEWIGWIYPGNVNTKY 79

Qy   61 NEKFKGKATLTADKSSTAYMQLSSLTSDDSAVYFCARD--GPWFAYWGQGTLVTVSA 116
        |||||||||||||||||||||||||||||:|||| | |||||||||||||||
Db   80 NEKFKGKATLTADKSSTAYMQLSSLTSEDSAVFCARNYGSSYCLAYWGQGTLVTVSA 138

RESULT 12
S38950
Ig gamma chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S38950
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A;Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp
A;Reference number: S38950; MUID:9128242; PMID:8297501
A;Accession: S38950
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-246 <KLE>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;137-201/Domain: immunoglobulin homology <IMM>

Query Match   78.6%; Score 482.5; DB 2; Length 246;
Best Local Similarity 79.5%; Pred. No. 1.9e-36;
Matches 93; Conservative   7; Mismatches 16; Indels 1; Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        ||||||||:|||||| ||||| ||||||||:| ||||||:||||||| |:|||||:|
Db   1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGYIHWVKQRPGSGNTKY 60

Qy   61 NEKFKGKATLTADKSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
        |||||||||||:| :||||||||||||:||||||||| | :|||||||||:|||:
Db   61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYWGQGTSVTVSS 117

RESULT 13
S40295
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
A;Reference number: S40295
A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: v-D-J region <VDJ>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
F;l/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match   78.6%; Score 482.5; DB 2; Length 446;
Best Local Similarity 79.5%; Pred. No. 3.5e-36;
Matches 93; Conservative   7; Mismatches 16; Indels 1; Gaps 1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60

```
Db         |:|||||| |||||| |||||||||||||:|||:||||| ||||||:||||||| |||||| |
        1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY 60

Qy     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
          ||||||||||||||||||||||||||||||||||||||||||: ||||:
Db     61 NEKFKGKATLIVDTSSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYWGQGTSVTVSS 117
```

RESULT 14
E30562
Ig heavy chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C;Accession: E30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: E30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   78.4%;   Score 481.5;   DB 2;   Length 119;
Best Local Similarity   78.2%;   Pred. No. 1.1e-36;
Matches   93; Conservative   9;   Mismatches   14;   Indels   3;   Gaps   1;

```
Qy      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||||||||||:||:|||:||||||||:|||::|||||||||||||||: ||||
Db      1 QVQLQQSGAELMKPGASVKISCKATGYTFSSWIEWVKQRPGHGLEWIGEIFPGSGSTKY 60

Qy     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR--DGPWFAYWGQGTLVTVSA 116
          ||||||||||||:||||||||||||||||||||||||   :|||||||||||||||
Db     61 NEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARHYGSSSFAYWGQGTLVTVSA 119
```

RESULT 15
JL0076
Ig heavy chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: JL0076
R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A;Reference number: JL0076; MUID:89096973; PMID:3211160
A;Accession: JL0076
A;Molecule type: mRNA
A;Residues: 1-141 <KAA>
A;Cross-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-141/Product: Ig heavy chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;50-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;123-135/Region: J2 segment
F;136-141/Region: C

Query Match   78.3%;   Score 481;   DB 2;   Length 141;
Best Local Similarity   77.6%;   Pred. No. 1.4e-36;
Matches   90; Conservative   11;   Mismatches   15;   Indels   0;   Gaps   0;

```
Qy      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||||||||||:||:|||:|||||||||:||||||||||||||||||: ||||
Db     20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79

Qy     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
          ||||||||||||:||||||||||||||||||||||:||||||: |||||: :|||:
```

Db   80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAREGPAGDYWGQGTLTVSS 135

Search completed: August 16, 2004, 11:09:11
Job time : 13.4843 secs

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OM protein - protein search, using sw model

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                  GenCore version 5.1.6

Run on:  August 16, 2004, 11:08:06 ; Search time 8.32287 Seconds
                                     (without alignments)
                                     725.728 Million cell updates/sec

Title:          US-09-889-300A-1
Perfect score:  614
Sequence:       1 QVQLQQSGAELVRPGTSVKV.........ARDGPWFAYWGQGTLVTVSA 116

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:        141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	475.5	77.4	138	1	HV48_MOUSE	P03980 mus musculu
2	471.5	76.8	120	1	HV03_MOUSE	P01747 mus musculu
3	469.5	76.5	140	1	HV02_MOUSE	P01746 mus musculu
4	466	75.9	139	1	HV07_MOUSE	P01751 mus musculu
5	457	74.4	137	1	HV11_MOUSE	P01755 mus musculu
6	455.5	74.2	117	1	HV12_MOUSE	P01756 mus musculu
7	454.5	74.0	117	1	HV13_MOUSE	P01757 mus musculu
8	454.5	74.0	121	1	HV01_MOUSE	P01745 mus musculu
9	432	70.4	120	1	HV50_MOUSE	P06329 mus musculu
10	429	69.9	117	1	HV04_MOUSE	P01748 mus musculu
11	427	69.5	117	1	HV52_MOUSE	P06327 mus musculu
12	425	69.2	118	1	HV51_MOUSE	P06330 mus musculu
13	414	67.4	117	1	HV06_MOUSE	P01750 mus musculu
14	414	67.4	117	1	HV09_MOUSE	P01753 mus musculu
15	411	66.9	117	1	HV05_MOUSE	P01749 mus musculu
16	411	66.9	117	1	HV49_MOUSE	P06328 mus musculu
17	410	66.8	117	1	HV10_MOUSE	P01754 mus musculu
18	401.5	65.4	136	1	HV15_MOUSE	P01759 mus musculu
19	385	62.7	147	1	HV1C_HUMAN	P01744 homo sapien
20	384	62.5	117	1	HV14_MOUSE	P01758 mus musculu
21	368	59.9	117	1	HV1G_HUMAN	P23083 homo sapien
22	363	59.1	117	1	HV1B_HUMAN	P01743 homo sapien
23	356	58.0	114	1	HV00_MOUSE	P01741 mus musculu
24	332.5	54.2	117	1	HV1A_HUMAN	P01742 homo sapien
25	327	53.3	122	1	HV3G_HUMAN	P01768 homo sapien
26	324	52.8	119	1	HV37_MOUSE	P01807 mus musculu
27	320	52.1	119	1	HV40_MOUSE	P01810 mus musculu
28	316.5	51.5	121	1	HV3J_HUMAN	P01771 homo sapien
29	316	51.5	120	1	HV1H_HUMAN	P80421 homo sapien
30	314.5	51.2	142	1	HV01_RAT	P01805 rattus norv
31	312	50.8	119	1	HV38_MOUSE	P01808 mus musculu
32	309.5	50.4	119	1	HV3I_HUMAN	P01770 homo sapien
33	308.5	50.2	115	1	HV32_MOUSE	P01801 mus musculu
34	308.5	50.2	117	1	HV17_MOUSE	P01786 mus musculu
35	308.5	50.2	117	1	HV41_MOUSE	P01811 mus musculu
36	308.5	50.2	125	1	HV1F_HUMAN	P06326 homo sapien
37	305.5	49.8	117	1	HV42_MOUSE	P01812 mus musculu
38	304.5	49.6	118	1	HV39_MOUSE	P01809 mus musculu
39	303.5	49.4	113	1	HV30_MOUSE	P01799 mus musculu
40	303	49.3	136	1	HV16_MOUSE	P01783 mus musculu
41	301	49.0	126	1	HV3K_HUMAN	P01772 homo sapien
42	300.5	48.9	115	1	HV33_MOUSE	P01802 mus musculu
43	299	48.7	114	1	HV01_CANFA	P01784 canis famil
44	299	48.7	114	1	HV3B_HUMAN	P01763 homo sapien
45	298.5	48.6	113	1	HV27_MOUSE	P01796 mus musculu

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                              ALIGNMENTS

RESULT 1
HV48_MOUSE
ID   HV48_MOUSE     STANDARD;      PRT;   138 AA.
AC   P03980;
DT   23-OCT-1986 (Rel. 02, Created)
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region TEPC 1017 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL         1     20
FT   CHAIN         21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN        21     49       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        50     54       FRAMEWORK-1.
FT   DOMAIN        55     68       FRAMEWORK-2.
FT   DOMAIN        69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        86    117       FRAMEWORK-3.
FT   DOMAIN       118    127       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       128    138       FRAMEWORK-4.
FT   DISULFID      41    115       BY SIMILARITY.
FT   NON_TER      138    138
SQ   SEQUENCE   138 AA;  15576 MW;  748157E4C6907B8E CRC64;

Query Match          77.4%;          Score 475.5;  DB 1;  Length 138;
Best Local Similarity   77.3%;        Pred. No. 6.3e-43;
Matches   92;  Conservative   8;  Mismatches  16;  Indels   3;  Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
         ||||||| |||| || || |||||| | ||||   ||||||||||||||||| |||| |
Db  20 QVQLQQFGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY 79

Qy  61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR-DG--PWFAYWGQGTLVTVSA 116
         ||||| ||||| ||||||||||||:  ||  ||||    ::  |  ||||||||||||
Db  80 NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDGYDWFVYWGQGTLVFSA 138

RESULT 2
HV03_MOUSE
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ID   HV03_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC       DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC       CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC       SEGMENT, JH2.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Hybridoma.
FT   DOMAIN        1    111       IG-LIKE.
FT   NON_TER       1
FT   NON_TER     120
SQ   SEQUENCE   120 AA;   13307 MW;   FF04E4A167B654AF CRC64;

Query Match             76.8%;   Score 471.5;   DB 1;   Length 120;
Best Local Similarity   76.7%;   Pred. No. 1.4e-42;
Matches   92;  Conservative   8;  Mismatches  15;  Indels   5;  Gaps    1;

Qy      2  VQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNYN  61
           |:||:|||||||| ||||||||||||:|||||||:||||||||||||||||||:||:|||
Db      1  VQLQQSGAELVRAGSSVRMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN  60

Qy     62  EKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD-----GPWFAYWGQGTLVTVSA  116
           ||||||| ||:|||||||||||||||||||||||||        ||:||||||||:|||
Db     61  EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYFDYWGQGTTLTVSS  120

RESULT 3
HV02_MOUSE
ID   HV02_MOUSE     STANDARD;      PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 93G7 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A94264; HVMSG7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Hybridoma; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    140       IG HEAVY CHAIN V REGION 93G7.
FT   DOMAIN       20    139       IG-LIKE.
FT   NON_TER     140
SQ   SEQUENCE   140 AA;   15514 MW;   254ACBBE31DA5CE8 CRC64;

Query Match             76.5%;   Score 469.5;   DB 1;   Length 140;
Best Local Similarity   76.9%;   Pred. No. 2.7e-42;
Matches   93;  Conservative   9;  Mismatches  14;  Indels   5;  Gaps    2;

Qy      1  QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY  60
            :||||||||||||| |||||||||||||:||||||||||||||||||||||||||:||
Db     20  EVQLQQSGAELVRAGSSVRMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY  79

Qy     61  NEKFKPGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD----GPW-FAYWGQGTLVTVS  115
           |||||||||||||:|||||||||||||||||||||||||       ||| :|||||||||:
Db     80  NEKFKPGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYGGSYDFDYWGQGTPLTVS  139

Qy    116  A  116
              :
Db    140  S  140

RESULT 4
HV07_MOUSE
ID   HV07_MOUSE     STANDARD;      PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region B1-8/186-2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., PasKind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A90809; MHMS18.
DR   PDB; 1A6U; 27-MAY-98.
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Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
         |:|||||||| |||||||| ||||||||||||||||| |:||| ||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGAGTTVTVSS 117

RESULT 7
ID   HV13_MOUSE    STANDARD;    PRT;    117 AA.
AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region J558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC       BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC       WHICH OCCUR IN THE D AND J SEGMENTS.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A26242; MHMSJ5.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS0835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    116       IG-LIKE.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;   13024 MW;  292E2AF4BE447E81 CRC64;

Query Match         74.0%;  Score 454.5;  DB 1;  Length 117;
Best Local Similarity   73.5%;  Pred. No. 8.3e-41;
Matches    86;  Conservative   14;  Mismatches   16;  Indels    1;  Gaps    1;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          :|||||||||||||||||||||||||||||||||||:||||||||||||||||:||| :
Db    1 EVQLQQSGPELVKPGASVRMSCKASGYTFTDYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
         |:|||||||| |||||||| ||||||||||||||| |:||| ||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYWYFDVWGAGTTVTVSS 117

RESULT 8
ID   HV01_MOUSE    STANDARD;    PRT;    121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable
RT   region of immunoglobulin heavy chain MPC11.";
```

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RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC       FROM A MYELOMA THAT SECRETES IGG2B.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A93708; GVMS11.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS0835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       IG-LIKE.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;   13135 MW;  227AEF3EC56ED0BF CRC64;

Query Match         74.0%;  Score 454.5;  DB 1;  Length 121;
Best Local Similarity   71.9%;  Pred. No. 8.7e-41;
Matches    87;  Conservative   11;  Mismatches   18;  Indels    5;  Gaps    1;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          : ||||||||||||||||||||||||||||||||:||||||||||||||||:|||||| :
Db    1 EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR----DGPWFAYWGQGTLVTVS 115
         |:| |||||||||||||:|||||||:||||||||||| |:|||||||||
Db   61 NDNLKGKATLTADTSSSTAYLQLSSLTSEDCAIYHCARGIYYNSPYFDWGGQGTTLVTVS 120

Qy  116 A 116
Db  121 S 121

RESULT 9
ID   HV50_MOUSE    STANDARD;    PRT;    120 AA.
AC   P06329;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region AC38 15.3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02037; MHMS15.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS0835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     98       V SEGMENT.
FT   DOMAIN       99    105       D SEGMENT.
FT   DOMAIN      106    120       J SEGMENT.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;   13311 MW;  914453F426F09834 CRC64;

Query Match         70.4%;  Score 432;  DB 1;  Length 120;
Best Local Similarity   69.2%;  Pred. No. 2e-38;
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Matches    83;  Conservative  13;  Mismatches  20;  Indels   4;  Gaps   2;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        |||||||||||||||||||||||||||||||||||:||||||||::|||||||||||||
Db    1 QVQLLQPGTELVKPGASVNLSCKASGYTFTSYWMHWIRQRPGQGLEWIGIGINPSNGGTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR---DGP-WFAYWGQGTLVTVSA 116
        |||||||||||||||||||||||||||||||||||||:  :|| :||||||||||||||:
Db   61 NEKFKSKATLTVDKSSSATYMQLSTPSEDSAVYYCARWDYEGDRYFDVWGTGTTVTVSS 120

RESULT 10
HV04_MOUSE
ID   HV04_MOUSE          STANDARD;       PRT;   117 AA.
AC   P01748;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 23 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; A02030; HVMS23.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 23.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12772 MW;  C530F829C906F693 CRC64;

Query Match             69.9%;  Score 429;  DB 1;  Length 117;
Best Local Similarity   81.6%;  Pred. No. 3.9e-38;
Matches    80;  Conservative   7;  Mismatches  11;  Indels   0;  Gaps   0;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        |||||||||||||||||||||||||||||||||||:||||||||::|||||||||||||
Db   20 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPGNGGTNY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR 98
        |||||||||||||:||||||||||||||||||||
Db   80 NEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYYCAR 117

RESULT 11
HV52_MOUSE
ID   HV52_MOUSE          STANDARD;       PRT;   117 AA.
AC   P06327;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
```

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DE   Ig heavy chain V region VH558 A1/A4 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; M13787; AAA38439.1; -.
DR   PIR; A02029; HVMSA1.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION VH558 A1/A4.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12971 MW;  8B0BC138856DFC9D CRC64;

Query Match             69.5%;  Score 427;  DB 1;  Length 117;
Best Local Similarity   83.7%;  Pred. No. 6.4e-38;
Matches    82;  Conservative   5;  Mismatches  11;  Indels   0;  Gaps   0;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        |||||||||||||||||||||||||||||||||||:||||||||::|||||||||||||
Db   20 QVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPGQGLEWIGWIYPGDGSTKY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR 98
        |||||||||||||||||||||||||||||||||
Db   80 NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117

RESULT 12
HV51_MOUSE
ID   HV51_MOUSE          STANDARD;       PRT;   118 AA.
AC   P06330;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region AC38 205.12.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
```

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DR   PIR; A02040; MHMS38.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig;1.
DR   SMART; SM004O6; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        9     98      V SEGMENT.
FT   DOMAIN       99    104      D SEGMENT.
FT   DOMAIN      105    118      J SEGMENT.
FT   DISULFID     22     96      BY SIMILARITY.
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  12934 MW;  94F7BEE4C762A018 CRC64;

Query Match             69.2%;  Score 425; DB 1; Length 118;
Best Local Similarity   68.6%;  Pred. No. 1e-37;
Matches    81;  Conservative   14;  Mismatches   21;  Indels    2;  Gaps    1;

Qy     1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
           ||||||:||:|||||:|||||||||||||||| :|||||||||||||||:|||:||
Db     1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYMNWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy    61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
           |:||||||||.|||.||::||||:|||:||.:||.||
Db    61 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARGYGYDPFDVWGTGTTVTVSS 118

RESULT 13
HV06_MOUSE
ID   HV06_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01750;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 102 precursor.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57Bl/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; A02032; HVMS02.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig;1.
DR   SMART; SM004O6; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117      IG HEAVY CHAIN V REGION 102.
FT   DOMAIN       20     49      FRAMEWORK-1.
FT   DOMAIN       50     54      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68      FRAMEWORK-2.
FT   DOMAIN       69     85      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117      FRAMEWORK-3.
FT   DISULFID     41    115      BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12867 MW;  740A65DD851FCA8C CRC64;

Query Match             67.4%;  Score 414; DB 1; Length 117;
Best Local Similarity   81.2%;  Pred. No. 1.5e-36;
Matches    78;  Conservative    7;  Mismatches   11;  Indels    0;  Gaps    0;
```

```
Qy     2 VQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNYN 61
           ||||||||||||:||:|||||||||||||||| ::||||||||||||||||| |:|||
Db    21 VQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHVKQRPGQGLEWIGRIHPSDSDTNYN 80

Qy    62 EKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCA 97
           :||||||||.|||:||||||||||||:||:||||||
Db    81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

RESULT 14
HV09_MOUSE
ID   HV09_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01753; P11271;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 186-1 precursor.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57Bl/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; D90809; HVMS61.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM004O6; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117      IG HEAVY CHAIN V REGION 186-1.
FT   DOMAIN       20     49      FRAMEWORK-1.
FT   DOMAIN       50     54      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68      FRAMEWORK-2.
FT   DOMAIN       69     85      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117      FRAMEWORK-3.
FT   DISULFID     41    115      BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12890 MW;  16191A08CB17F5A CRC64;

Query Match             67.4%;  Score 414;  DB 1;  Length 117;
Best Local Similarity   79.6%;  Pred. No. 1.5e-36;
Matches    78;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
           ||||||||||||:||:|||||||||||||||| ::||||||||||:||| |:||
Db    20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHVKQRPGRGLEWIGRIDPNSGGTKY 79

Qy    61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR 98
           |:||||||||.|||:|||||||||||||:||:||||||
Db    80 NEKFKSKATLIVDTSSSTAYMQLHSLTSEDSAVYYCAR 117

RESULT 15
HV05_MOUSE
ID   HV05_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01749;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ig heavy chain V region 3 precursor.
```

```
GN   IGH-VJ558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; J00536; AAA38605.1; -.
DR   PIR; A02031; HVMS3.
DR   HSSP; P01810; 2FBJ.
DR   MGD; MGI:96486; Igh-VJ558.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 3.
FT   DOMAIN       20     49       FRAMEWORK-1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     68       FRAMEWORK-2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       86    117       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13016 MW;  427C861C53975EDC CRC64;
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Query Match           66.9%;   Score 411;  DB 1;  Length 117;
Best Local Similarity 79.6%;   Pred. No. 3e-36;
Matches   78;  Conservative   9;  Mismatches   11;  Indels   0;  Gaps   0;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||||||||||||| ||||||||||||||||||||| | : ||||||||||||||| | :|
Db   20 QVQLQQPGAELVRPGSSVKLSCKASGYTFTSYWMDWVKQRPGQGLEWIGNIYPDSETHY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR 98
          |:||| |||||| ||||||||||||||||||: |||||:||
Db   80 NQKFKDKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR 117
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Search completed: August 16, 2004, 11:08:35
Job time : 8.32287 secs

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          GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:        August 16, 2004, 11:08:06 ; Search time 34.3318 Seconds
                                            (without alignments)
                                            1066.069 Million cell updates/sec

Title:         US-09-889-300A-1
Perfect score: 614
Sequence:      1 QVQLQQSGAELVRPGTSVKV........ARDGPWFAYWGQGTLVTVSA 116

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:     1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     SPTREMBL_25:*
          1: sp_archea:*
          2: sp_bacteria:*
          3: sp_fungi:*
          4: sp_human:*
          5: sp_invertebrate:*
          6: sp_mammal:*
          7: sp_mhc:*
          8: sp_organelle:*
          9: sp_phage:*
         10: sp_plant:*
         11: sp_rodent:*
         12: sp_virus:*
         13: sp_vertebrate:*
         14: sp_unclassified:*
         15: sp_rvirus:*
         16: sp_bacteriap:*
         17: sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	526.5	85.7	473	11	Q9D8L4	mus musculu
2	484.5	78.9	614	11	Q7TMT6	mus musculu
3	483.5	78.7	142	11	Q924Q1	mus musculu
4	477	77.7	463	11	Q99LC4	mus musculu
5	475	77.4	143	11	Q924Q0	mus musculu
6	472.5	77.0	481	11	Q91WT1	mus musculu
7	471	76.7	482	11	Q8K172	mus musculu
8	470.5	76.6	489	11	Q8VCX4	mus musculu
9	470	76.5	145	11	Q924P7	mus musculu
10	467	76.2	613	11	Q8VCX7	mus musculu
11	467	76.1	141	11	Q924Q4	mus musculu
12	466.5	76.0	140	11	Q924P8	mus musculu
13	466	75.9	145	11	Q924R3	mus musculu
14	466	75.9	145	11	Q924Q7	mus musculu
15	466	75.9	145	11	Q924R1	mus musculu
16	463	75.4	139	11	Q924R5	mus musculu
17	462.5	75.3	146	11	Q924R8	mus musculu
18	462.5	75.3	480	11	Q8K0Z4	mus musculu
19	462	75.2	143	11	Q924R0	mus musculu
20	461	75.1	137	11	Q924R6	mus musculu
21	461	75.1	145	11	Q924Q6	mus musculu
22	460.5	75.0	146	11	Q924Q8	mus musculu
23	460	74.9	143	11	Q924Q5	mus musculu
24	460	74.9	145	11	Q91V67	mus musculu
25	460	74.9	143	11	Q924Q9	mus musculu
26	458.5	74.7	117	11	Q9QXF0	mus musculu
27	458.5	74.7	146	11	Q924Q3	mus musculu
28	458	74.6	278	11	Q921K1	mus musculu
29	457.5	74.5	140	11	Q924R2	mus musculu
30	457	74.4	118	11	Q971C4	mus musculu
31	457	74.4	145	11	Q924R4	mus musculu
32	456	74.3	481	11	Q8VCV5	mus musculu
33	453.5	73.9	117	11	Q9QXE9	mus musculu
34	453.5	73.9	144	11	Q924P5	mus musculu
35	453	73.8	473	11	Q99L25	mus musculu
36	452	73.6	143	11	Q924R7	mus musculu
37	449	73.1	109	11	Q9JL75	mus musculu
38	449	73.1	143	11	Q924P9	mus musculu
39	448.5	73.0	120	11	Q920E8	mus musculu
40	447	72.8	143	11	Q91VA2	mus musculu
41	446.5	72.7	168	11	Q8VDC9	mus musculu
42	445.5	72.6	123	11	Q8VIJ1	mus musculu
43	445	72.5	488	11	Q91WR1	mus musculu
44	442	72.0	136	11	Q7TPE3	mus musculu
45	438	71.3	143	11	Q924P6	mus musculu

ALIGNMENTS

```
RESULT 1
Q9D8L4
ID   Q9D8L4        PRELIMINARY;      PRT;    473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1810060009Rik protein.
GN   IGH-1 OR 1810060009RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez J., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK007918; BAB25349.1; -.
DR   PIR; S26746; S26746.
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DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96443; Igh-1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE  473 AA;  51699 MW;  9DED57A514475FBB CRC64;

Query Match           85.7%;  Score 526.5;  DB 11;  Length 473;
Best Local Similarity  84.9%;  Pred. No. 2.5e-46;
Matches  101;  Conservative   5;  Mismatches  10;  Indels   3;  Gaps  1;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        |||||||||||||||||:|||||||||||||||| |||||| :||||||||||:|:||
Db   20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYINWVKQRPGQGLEWIGKIGPGSGSTYY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDG---PWFAYWGQGTLVTVSA 116
        ||||||||||||||||||||||||||||||||||||||||   |:||||||||||||||
Db   80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYWGQGTLVTVSA 138

RESULT 2
Q7TMT6
ID   Q7TMT6          PRELIMINARY;         PRT;   614 AA.
AC   Q7TMT6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053409; AAH53409.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE  614 AA;  67746 MW;  839BAF3B8D124F89 CRC64;

Query Match           78.9%;  Score 484.5;  DB 11;  Length 614;
Best Local Similarity  79.8%;  Pred. No. 8.3e-42;
Matches   95;  Conservative   8;  Mismatches  13;  Indels   3;  Gaps  1;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        |||||||||||||||||:||||||||||||||||||||||||||:|| ::|||||||||||
Db   20 QVQLQQSGPELVKPGASVKISCKASGYAFSSSWMNWVKQRPGKGLEWIGRVYPGDGDTNY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD---GPWFAYWGQGTLVTVSA 116
        |:|||||||||||||||||||||||||||||||||||||   |:||||||||||||||||
Db   80 NGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDYGSSYRFAYWGQGTLVTVSA 138

RESULT 3
Q924Q1
ID   Q924Q1          PRELIMINARY;         PRT;   142 AA.
AC   Q924Q1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   V23-D-J-C mu protein (Fragment).
GN   V23-D-J-C MU.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP)";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069913; BAB63929.1; -.
DR   PIR; F33932; F33932.
DR   PIR; I28833; I28833.
DR   PIR; PH1156; PH1156.
DR   PIR; PH1158; PH1158.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; IGv; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER    1      1
FT   NON_TER  142    142
SQ   SEQUENCE  142 AA;  15622 MW;  24A265CE4EA4318B CRC64;

Query Match           78.7%;  Score 483.5;  DB 11;  Length 142;
Best Local Similarity  79.7%;  Pred. No. 1.6e-42;
Matches   94;  Conservative   8;  Mismatches  13;  Indels   3;  Gaps  2;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
        |||||||||||||||||:||||||||||||||||||||||||||:|| ::|||||||||||
Db    1 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPSNGGTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGGGTLVTVSA 116
        |:|||||||||||||||||||||||||||||||||||||||::   |||||||||||:|
Db   61 NEKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARRG-WEAMDYWQGTSVTVSS 117

RESULT 4
Q99LC4
ID   Q99LC4          PRELIMINARY;         PRT;   463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to RIKEN cDNA 1810060009 gene.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
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RL  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; BC003435; AAH03435.1; -.
DR  PIR; B45837; B45837.
DR  HSSP; P01842; 7FAB.
DR  MGD; MGI:96646; Igh-4.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 3.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS50835; IG_LIKE; 4.
DR  PROSITE; PS00290; IG_MHC; 1.
SQ  SEQUENCE  463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;

Query Match             77.7%;  Score 477;  DB 11;  Length 463;
Best Local Similarity   77.5%;  Pred. No. 3.5e-41;  -
Matches   93;  Conservative   7;  Mismatches  16;  Indels   4;  Gaps   1;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          |||||||||||||||||||| : |||||||||||||||||:||||||:|||||||||
Db   20 QVQLQQSGAELARPGASVRLSCKASGYTFTGYGVSWVKQRTGQGLEWVGEIYPGSGNTY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW----FAYWGQGTLVTVSA 116
          :|||||||||||||||||||||||||||||||||||        |||||||||||||
Db   80 SEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSSYSYSYDLFAYWGQGTLVTVSA 139

RESULT 5
Q924Q0
ID  Q924Q0           PRELIMINARY;      PRT;   143 AA.
AC  Q924Q0;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  V165-D-J-C mu protein (Fragment).
GN  V165-D-J-C MU.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6;
RA  Kozono Y., Kozono H., Azuma T.;
RT  "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT  Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT  Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AB069915; BAB63931.1; -.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 1.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
FT  NON_TER      1      1
FT  NON_TER    143    143
SQ  SEQUENCE  143 AA;  15704 MW;  C99D2433F2BAD8A0 CRC64;

Query Match             77.4%;  Score 475;  DB 11;  Length 143;
Best Local Similarity   78.0%;  Pred. No. 1.3e-41;  -
Matches   92;  Conservative   8;  Mismatches  16;  Indels   2;  Gaps   1;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||||| |||||||||||||:|||||||||||||:||:||||||||||:|||||||||
Db    1 QVQLQQQPGAELVKPGASVKMSCKASGYTFTSYWITWVKQRPGQGLEWIGDIYPGSGSTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGP--WFAYWGQGTLVTVSA 116
          |||||:|||||:|||||||||||||||||:|||||:|      :| |||||||||||
Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAPDSNLYFDYWGQGTTLTVSS 118

RESULT 6
Q91WT1
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ID  Q91WT1           PRELIMINARY;      PRT;   481 AA.
AC  Q91WT1;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  Hypothetical protein.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Colon;
RA  Strausberg R.;
RL  Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; BC013490; AAH13490.1; -.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; ig; 4.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS50835; IG_LIKE; 4.
DR  PROSITE; PS00290; IG_MHC; 2.
KW  Hypothetical protein.
SQ  SEQUENCE  481 AA;  52105 MW;  97DF68D159463F65 CRC64;

Query Match             77.0%;  Score 472.5;  DB 11;  Length 481;
Best Local Similarity   77.8%;  Pred. No. 1.1e-40;  -
Matches   91;  Conservative   6;  Mismatches  19;  Indels   1;  Gaps   1;

Qy    1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          |||||||| ||||:||:|||:||||||||||:::|:|||||||| |||||:||:||:|||
Db   20 QVQLQQSGPELVKPGASVKISCKASGYTFTSYIHWVKQRPGQGLVWIGWIYPGDGNTKY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
          |||||||:|||||||||||||:|||||||:|||||||: |   ::| |||||||||:
Db   80 NEKFKGKTTLTADKSSSTAYMFLSSLTSEDSAVYFCTRGGGWAFDYWGQGTTLTVSS 136

RESULT 7
Q8K172
ID  Q8K172           PRELIMINARY;      PRT;   482 AA.
AC  Q8K172;
DT  01-OCT-2002 (TrEMBLrel. 22, Created)
DT  01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  Similar to expressed sequence AI893585.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Breast tumor;
RA  Strausberg R.;
RL  Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; BC028249; AAH28249.1; -.
DR  PIR; F33932; F33932.
DR  PIR; PH1105; PH1105.
DR  PIR; PH1108; PH1108.
DR  PIR; PH1114; PH1114.
DR  PIR; PH1118; PH1119.
DR  PIR; PH1119; PH1125.
DR  PIR; PH1125; PH1126.
DR  PIR; PH1126; PH1128.
DR  PIR; PH1128; PH1131.
DR  PIR; PH1131; PH1134.
DR  PIR; PH1134; PH1139.
DR  PIR; PH1139; PH1142.
DR  PIR; PH1142; PH1149.
DR  PIR; PH1149; PH1150.
DR  PIR; PH1150; PH1151.
DR  PIR; PH1151;
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DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00407; IGc1; 3.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
SQ   SEQUENCE   482 AA;  52121 MW;  A06FF083E771D084 CRC64;

Query Match             76.7%;  Score 471;  DB 11;  Length 482;
Best Local Similarity   76.3%;  Pred. No. 1.6e-40;
Matches    90;  Conservative   11;  Mismatches   15;  Indels    2;  Gaps    1;

Qy          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
              |||||||||||| : ||||||||||| :| : | |||||||||||||||||| : | | ||
Db         20 QVQLQQPGAELVRPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 79

Qy         61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFA--YWGQGTLVTVSA 116
              ||||| |||||||||  :|||||||||||||| : | |     ::  :|||||| ||||
Db         80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCTREGDYDAMDYWGQGTSVTVSS 137
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RESULT 8
Q8VCX4
ID   Q8VCX4                 PRELIMINARY;       PRT;   489 AA.
AC   Q8VCX4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-VJ558 OR AI893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018322; AAH18322.1; -.
DR   MGD; MGI:96486; Igh-VJ558.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   489 AA;  53208 MW;  CC85B1194DAFEF2C CRC64;

Query Match             76.6%;  Score 470.5;  DB 11;  Length 489;
Best Local Similarity   72.8%;  Pred. No. 1.8e-40;
Matches    91;  Conservative    9;  Mismatches   16;  Indels    9;  Gaps    2;

Qy          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
              :|||||||||||| : ||||||||||| :| : | |||||||||||| :| | | | ||
Db         20 KVQLQQSGAELVRPGASVKLSCKASGYTFSDYFIHWIKQRSGQGLEWIGWFNPGSGSIKF 79

Qy         61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR------DG--PWFAYWGQGTL 111
              ||||| |||||  |  :||||||||||| :|||||||||      :|    |  |||||
Db         80 NEKFKDKATLTADKSSTTVYMDLSRLTSEDSAVYFCARHEDRGNYDGSLAWFVYWGQGTL 139

Qy        112 VTVSA 116
              |||||
Db        140 VTVSA 144
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RESULT 9
Q924P7
ID   Q924P7                 PRELIMINARY;       PRT;   145 AA.
AC   Q924P7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069918; BAB63934.1; -.
DR   PIR; F28833; F28833.
DR   PIR; F33932; F33932.
DR   PIR; PH105; PH105.
DR   PIR; PH114; PH114.
DR   PIR; PH118; PH118.
DR   PIR; PH119; PH119.
DR   PIR; PH125; PH125.
DR   PIR; PH126; PH126.
DR   PIR; PH128; PH128.
DR   PIR; PH134; PH134.
DR   PIR; PH137; PH137.
DR   PIR; PH142; PH142.
DR   PIR; PH149; PH149.
DR   PIR; PH150; PH150.
DR   PIR; PH151; PH151.
DR   PIR; PH152; PH152.
DR   PIR; PH153; PH153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1
FT   NON_TER     145     145
SQ   SEQUENCE   145 AA;  15988 MW;  FB73958704796C9A CRC64;

Query Match             76.5%;  Score 470;  DB 11;  Length 145;
Best Local Similarity   77.5%;  Pred. No. 4.3e-41;
Matches    93;  Conservative    9;  Mismatches   14;  Indels    4;  Gaps    2;

Qy          1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
              |||||||||||| : ||||||||||| :| : | ||| :: :| |||||||||||||||
Db          1 QVQLQQPGAELVRPGSSVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy         61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR-DGPWF---AYWGQGTLVTVSA 116
              ||||| |||||||| : ||||||||||||:|||||||| | |     |:|||||||||||
Db         61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARKDGSSFYAMDYWGQGTSVTVSS 120
```

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RESULT 10
Q8VCX7
ID   Q8VCX7                 PRELIMINARY;       PRT;   613 AA.
AC   Q8VCX7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   IGH-6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
```

RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018315; AAH18315.1; -.
DR   MGD; MGI:96448; Igh-6.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; 3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;   67855 MW;   41A9384DD4C22862 CRC64;

Query Match   76.2%; Score 468; DB 11; Length 613;
Best Local Similarity   77.1%; Pred. No. 4.3e-40;
Matches   91; Conservative 10; Mismatches 15; Indels   2; Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
           |||||||||||:|| ||||:||:||||:|:|| |||||||||||||| |:| ||||
Db   20 QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNY 79

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARD-GPW-FAYWGQGTLVTVSA 116
           ||||||||||| ||||||||||||||:||||||||| ||||| |:|||:||||||
Db   80 NEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARRLGRWYFDVWGAGTTVTVSS 137

RESULT 11
Q924Q4
ID   Q924Q4   PRELIMINARY;   PRT;   141 AA.
AC   Q924Q4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [1]
DR   EMBL; AB067796; BAB63281.1; -.
DR   PIR; F28833, F28833.
DR   PIR; PH1105, PH1105.
DR   PIR; PH1108, PH1108.
DR   PIR; PH1114, PH1114.
DR   PIR; PH1118, PH1118.
DR   PIR; PH1119, PH1119.
DR   PIR; PH1125, PH1125.
DR   PIR; PH1126, PH1126.
DR   PIR; PH1128, PH1128.
DR   PIR; PH1129, PH1129.
DR   PIR; PH1131, PH1131.
DR   PIR; PH1134, PH1134.
DR   PIR; PH1137, PH1137.
DR   PIR; PH1139, PH1139.
DR   PIR; PH1142, PH1142.
DR   PIR; PH1144, PH1144.
DR   PIR; PH1147, PH1147.
DR   PIR; PH1149, PH1149.
DR   PIR; PH1150, PH1150.
DR   PIR; PH1151, PH1151.
DR   PIR; PH1152, PH1152.
DR   PIR; PH1153, PH1153.

DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   141   141
SQ   SEQUENCE   141 AA;   15561 MW;   DDB0482D66B76A0 CRC64;

Query Match   76.1%; Score 467; DB 11; Length 141;
Best Local Similarity   75.9%; Pred. No. 8.5e-41;
Matches   88; Conservative 11; Mismatches 17; Indels   0; Gaps   0;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
           |||||||||||| |||:|| ||||:|:|| ||||||||||||||| |:| ||||
Db   1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPWFAYWGQGTLVTVSA 116
           ||||||||||| ||||||||||||||:|||||||| ||:| |||||:||||
Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARDDYGRTFWGQGTTLTVSS 116

RESULT 12
Q924P8
ID   Q924P8   PRELIMINARY;   PRT;   140 AA.
AC   Q924P8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   V23-D-J-C mu protein (Fragment).
GN   V23-D-J-C MU.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069917; BAB63933.1; -.
DR   PIR; I28833; I28833.
DR   PIR; PH1156; PH1156.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   140   140
SQ   SEQUENCE   140 AA;   15392 MW;   904C80C82548C936 CRC64;

Query Match   76.0%; Score 466.5; DB 11; Length 140;
Best Local Similarity   76.9%; Pred. No. 9.5e-41;
Matches   90; Conservative 10; Mismatches 14; Indels   3; Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
           ||||||| |||:||||:||:||:||||:|:|| ||||||||||||||| ||| ||||
Db   1 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPSNGGTNY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARDGPW-FAYWGQGTLVTVSA 116
           ||||||||||| |||||||||:||:||:||||||||||| | :|||||||:
Db   61 NEKFKSKATLTVDKSSSTACTQLSSLTSEDSAVYYCARN-WDFDYWGQGTTLTVSS 115

RESULT 13
Q924R3
ID   Q924R3   PRELIMINARY;   PRT;   145 AA.
AC   Q924R3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)

RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067793; BAB63278.1; -.
DR   PIR; F28833; F28833.
DR   PIR; PH1105; PH1105.
DR   PIR; PH1108; PH1108.
DR   PIR; PH1114; PH1114.
DR   PIR; PH1118; PH1118.
DR   PIR; PH1119; PH1119.
DR   PIR; PH1125; PH1125.
DR   PIR; PH1126; PH1126.
DR   PIR; PH1128; PH1128.
DR   PIR; PH1129; PH1129.
DR   PIR; PH1131; PH1131.
DR   PIR; PH1134; PH1134.
DR   PIR; PH1137; PH1137.
DR   PIR; PH1139; PH1139.
DR   PIR; PH1142; PH1142.
DR   PIR; PH1144; PH1144.
DR   PIR; PH1147; PH1147.
DR   PIR; PH1149; PH1149.
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   145   145
SQ   SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match   75.9%; Score 466; DB 11; Length 145;
Best Local Similarity   74.2%; Pred. No. 1.1e-40;
Matches   89; Conservative 11; Mismatches 16; Indels   4; Gaps   1;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
           |||||| ||||||||||||||||:|||||||||:|::|||||||||||||| || || |
Db   1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR---DGPFAYWGQGTLVTVSA 116
            ||||||||| ||| | |||||||| |||||||:| || ||:||||||||:
Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYCARYDYGSSYFDYWGQGTTLTVSS 120

RESULT 15
Q924R1
ID   Q924R1
AC   Q924R1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update).
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067787; BAB63272.1; -.
DR   PIR; F28833; F28833.
DR   PIR; PH1105; PH1105.
DR   PIR; PH1108; PH1108.
DR   PIR; PH1114; PH1114.
DR   PIR; PH1118; PH1118.
DR   PIR; PH1119; PH1119.
DR   PIR; PH1125; PH1125.
DR   PIR; PH1126; PH1126.
DR   PIR; PH1128; PH1128.
DR   PIR; PH1129; PH1129.
DR   PIR; PH1131; PH1131.
DR   PIR; PH1134; PH1134.
DR   PIR; PH1137; PH1137.
DR   PIR; PH1139; PH1139.
DR   PIR; PH1142; PH1142.
DR   PIR; PH1144; PH1144.
DR   PIR; PH1147; PH1147.
DR   PIR; PH1149; PH1149.
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   PIR; S26744; S26744.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   145   145
SQ   SEQUENCE 145 AA; 15996 MW; 35B1A36B4280BA81 CRC64;

Query Match   75.9%; Score 466; DB 11; Length 145;
Best Local Similarity   75.8%; Pred. No. 1.1e-40;
Matches   91; Conservative   9; Mismatches 16; Indels   4; Gaps   2;

Qy   1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
           |||||| ||||||||||||||||:|||||||||:|::|||||||||||||| || || |
Db   1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy   61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR---DGPW-FAYWGQGTLVTVSS 116
            ||||||||| ||| | |||||||| |||||||:| :| ||:||||||||||
Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARGLYDGNWYFDVWGTGTTLTVSS 120

RESULT 14
Q924Q7
ID   Q924Q7
AC   Q924Q7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;

```
DR   EMBL; AB067789; BAB63274.1; -.
DR   PIR; F28833; F28833.
DR   PIR; F33932; F33932.
DR   PIR; PH1105; PH1105.
DR   PIR; PH1108; PH1108.
DR   PIR; PH1114; PH1114.
DR   PIR; PH1118; PH1118.
DR   PIR; PH1119; PH1119.
DR   PIR; PH1125; PH1125.
DR   PIR; PH1126; PH1126.
DR   PIR; PH1128; PH1128.
DR   PIR; PH1129; PH1129.
DR   PIR; PH1131; PH1131.
DR   PIR; PH1134; PH1134.
DR   PIR; PH1137; PH1137.
DR   PIR; PH1139; PH1139.
DR   PIR; PH1142; PH1142.
DR   PIR; PH1144; PH1144.
DR   PIR; PH1147; PH1147.
DR   PIR; PH1149; PH1149.
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
FT   NON_TER     145     145
SQ   SEQUENCE    145 AA;  15979 MW;  01G2D0A26C74G6CC04 CRC64;

Query Match            75.9%;  Score 466;  DB 11;  Length 145;
Best Local Similarity  76.7%;  Pred. No. 1.1e-40;
Matches   92;  Conservative   9;  Mismatches  15;  Indels   4;  Gaps   2;

Qy      1 QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKQRPGQGLEWIGVINPGSGGTNY 60
          ||||:||||||||| :||||||||||||||  :|:| :||||||| ::|||||| :|:||
Db      1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSSGGTKY 60

Qy     61 NEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR-DGPWF---AYWGQGTLVTVSA 116
          ||||:| ||||:|||||||||||||||||||||:|||| |||||    ||||||:||||:
Db     61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDGSSFYAMDYWGQGTSVTVSS 120


Search completed: August 16, 2004, 11:10:29
Job time : 36.3318 secs
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